

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 3, 2005, 08:08:21 ; Search time 3 Seconds  
(without alignments)  
481.084 Million cell updates/sec

Title: US-10-616-279-10

Perfect score: 85

Sequence: 1 HSSDYSWVRKNQYVS 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	54.1	438	1 ALEBH	alpha-amylase (EC
2	43.5	51.2	545	2 T40207	hypothetical prote
3	42	49.4	435	2 JC7137	alpha-amylase (EC
4	42	49.4	435	2 S12625	alpha-amylase (EC
5	42	49.4	729	2 C84854	ferric-coprogen re
6	42	49.4	729	2 H90813	outer membrane rec
7	42	49.4	729	2 D85673	outer membrane rec
8	42	49.4	877	2 S58824	probable membrane
9	42	49.4	1080	2 A71485	probable pbp2-tran
10	42	49.4	3587	2 I40486	surfactin syntheta
11	41	48.2	121	2 E97103	hypothetical prote
12	41	48.2	304	2 D82189	conserved hypothet
13	41	48.2	372	2 G89921	alanine dehydrogen
14	41	48.2	410	2 S77661	hypothetical prote
15	41	48.2	432	2 G90268	conserved hypothet
16	41	48.2	805	2 T34212	hypothetical prote
17	40	47.1	135	2 C21826	alpha-amylase (EC
18	40	47.1	153	2 A21826	alpha-amylase (EC
19	40	47.1	299	2 D82880	cytosine-specific
20	40	47.1	337	2 AD3614	glycosyl transfera
21	40	47.1	423	2 T09942	alpha-amylase (EC
22	40	47.1	427	1 ALEHB	alpha-amylase (EC
23	40	47.1	429	1 J50406	sensor protein Uhp
24	40	47.1	527	2 A82431	hypothetical prote
25	40	47.1	836	2 T42323	DNA-directed DNA p
26	40	47.1	1179	2 T35093	hypothetical prote
27	39	45.9	88	2 AF1023	hypothetical prote
28	39	45.9	111	2 B25159	13K sin operon hyp
29	39	45.9	279	2 D82243	transcription regu

30	39	45.9	379	2 T50967	probable pyruvate
31	39	45.9	425	2 S68305	gag polyprotein -
32	39	45.9	437	2 JC7138	alpha-amylase (EC
33	39	45.9	440	2 S14958	alpha-amylase (EC
34	39	45.9	446	2 H90063	hypothetical prote
35	39	45.9	494	2 T28660	probable adhesin p
36	39	45.9	568	2 T28876	hypothetical prote
37	39	45.9	1085	2 S55352	IFH1 protein - yea
38	39	45.9	1150	2 T15277	hypothetical prote
39	38	44.7	69	2 FC1257	alpha-amylase (EC
40	38	44.7	260	2 T22990	hypothetical prote
41	38	44.7	261	2 D86729	hypothetical prote
42	38	44.7	296	2 T12770	probable endonucle
43	38	44.7	347	2 T23944	hypothetical prote
44	38	44.7	393	2 S39383	cyclin CCL1 - years
45	38	44.7	415	2 B84544	probable WD-40 rep

ALIGNMENTS

RESULT 1

ALBH

alpha-amylase (EC 3.2.1.1) precursor - barley

C;Species: Hordeum vulgare (barley)

C;Date: 03-Aug-1984 #sequence\_revision 03-Aug-1984 #text\_change 09-Jul-2004

C;Accession: A00846; S65602

R;Rogers, J.C.; Millman, C.

J. Biol. Chem. 258, 8169-8174, 1983

A;Title: Isolation and sequence analysis of a barley alpha-amylase cDNA clone.

A;Reference number: A00846; MUID:83238423; PMID:6190808

A;Accession: A00846

A;Molecule type: mRNA

A;Residues: 1-438 <ROG>

A;Cross-references: UNIPROT:P00693; GB:J01236; NID:g166986; PIDN:AAA32929.1; PID:g166987

A;Experimental source: cv. Himalaya

R;Juge, N.; Rodenburg, K.W.; Guo, X.J.; Chairx, J.C.; Svensson, B.

FEBS Lett. 363, 299-303, 1995

A;Title: Isozyme hybrids within the protruding third loop domain of the barley alpha-amylase

A;Reference number: S65602; MUID:95255567; PMID:7737421

A;Accession: S65602

A;Molecule type: protein

A;Residues: 25-29 <JUG>

C;Comment: Production of this enzyme in barley is hormonally regulated. Germinating barle

C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycogen/starch degradation

C;Superfamily: wheat alpha-amylase; alpha-amylase core homology

C;Keywords: calcium binding; glycosidase; hydrolase; monomer; polysaccharide degradation

F;1-24/Domain: signal sequence #status predicted <Sig>

F;25-438/Product: alpha-amylase #status predicted <Sig>

F;171-318/Domain: alpha-amylase core homology <AMY>

F;204,229,315/Active site: Asp, Glu, Asp #status experimental

Query Match 54.1%; Score 46; DB 1; Length 438;

Best Local Similarity 54.5%; Pred. No. 9.7;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HSSDYSWVRKN 11

Db 419 HGNDYAVWEKN 429

RESULT 2

T40207

hypothetical protein SPBC31F10.04c - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C;Accession: T40207

R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Pohl, T.

submitted to the EMBL Data Library, August 1997

A;Reference number: T21913

A;Accession: T40207

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-545 <WOO>

A;Cross-references: UNIPROT:P87306; EMBL:Z97204; PIDN:CAB10081.1; GSPDB:GN00067; SPDB:SF

A;Experimental source: strain 972h-; cosmid c31f10

C;Genetics:

A;Gene: SPDB:SPBC31F10.04c

A;Map position: 2

A;Introns: 30/2; 113/2

Query Match 51.2%; Score 43.5; DB 2; Length 545;

Best Local Similarity 56.2%; Pred. No. 30;

Matches 9; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 HSSDYSWVR-KNQVVS 15

| | | | | | | | | | | | | | | |

Db 502 HGTDKSVWRCKDQYSS 517

RESULT 3

JC7137

N;Alternate names: 1,4-gulcan glucanohydrolase I

C;Species: Oryza sativa (rice)

C;Date: 04-Mar-2000 #sequence\_revision 04-Mar-2000 #text\_change 11-May-2000

C;Accession: JC7137; PC7039

R;Abe, R.; Yoshida, K.; Aoyagi, M.; Kasahara, S.; Ichishima, E.; Nakajima, T.

BioSci. Biotechnol. Biochem 63, 1329-1335, 1999

A;Title: Characterization of chimeric enzymes constructed between two distinct alpha-amyl

A;Reference number: JC7137; MUID:99430781; PMID:10500994

A;Accession: JC7137

A;Molecule type: mRNA

A;Residues: 1-435 <ABE>

A;Accession: PC7039

A;Molecule type: protein

A;Residues: 245-252 <AB2>

C;Comment: This enzyme catalyzes the hydrolysis of internal alpha-glucosidic linkages in

is important in germinating seeds and is present as multiple isoforms.

C;Genetics:

A;Gene: amy-I

C;Superfamily: wheat alpha-amylase; alpha-amylase core homology

C;Keywords: calcium binding; germination; glycosidase; hydrolase; seed

Query Match 49.4%; Score 42; DB 2; Length 435;

Best Local Similarity 60.0%; Pred. No. 42;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HSSDYSWVRK 10

| | | | |

Db 415 HGKDYSVWEK 424

RESULT 4

S12625

C;Species: Oryza sativa (rice)

C;Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 09-Jul-2004

C;Accession: S12625; S12776; S15054; JT0945

R;Huang, N.; Koizumi, N.; Reini, S.; Rodriguez, R.L.

Nucleic Acids Res. 18, 7007-7014, 1990

A;Title: Structural organization and differential expression of rice alpha-amylase genes

A;Reference number: JT0945; MUID:91088278; PMID:2263460

A;Accession: S12625

A;Molecule type: DNA

A;Residues: 1-435 <HUA>

A;Cross-references: UNIPROT:P27933; EMBL:M59351; NID:g169770; PIDN:AAA33895.1; PID:g1697

R;O'Neill, S.D.; Kumagai, M.H.; Majumdar, A.; Huang, N.; Sutliff, T.D.; Rodriguez, R.L.

Mol. Gen. Genet. 221, 235-244, 1990

A;Title: The alpha-amylase genes in Oryza sativa: characterization of cDNA clones and mR

A;Reference number: S12775; MUID:90318322; PMID:2370848

A;Accession: S12776

A;Molecule type: mRNA

A;Residues: 1-435 <ONE>

A;Cross-references: EMBL:M24287

R;O'Neill, S.D.; Kumagai, M.H.; Majumdar, A.; Huang, N.; Sutliff, T.D.; Rodriguez, R.L.

submitted to the EMBL Data Library, April 1989

A;Description: The alpha-amylase genes in Oryza sativa: Characterization of cDNA clones &

A;Reference number: S15054

A;Accession: S15054

A;Molecule type: mRNA

A;Residues: 1-72, 'R', 75-136, 'R', 138-435 <ON2>

A;Cross-references: EMBL:M24287; NID:g169754; PIDN:AAA33886.1; PID:g169755

C;Genetics:

A;Introns: 30/3; 342/3

C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycogen/starch degradation

C;Superfamily: wheat alpha-amylase; alpha-amylase core homology

C;Keywords: glycosidase; hydrolase; polysaccharide degradation

F;170-314/Domain: alpha-amylase core homology <AMY>

F;203,228,311/Active site: Asp, Glu, Asp #status predicted

Query Match 49.4%; Score 42; DB 2; Length 435;

Best Local Similarity 60.0%; Pred. No. 42;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HSSDYSWVRK 10

| | | | |

Db 415 HGKDYSVWEK 424

RESULT 5

C64854

ferric-coprogen receptor precursor - Escherichia coli (strain K-12)

N;Alternate names: outer membrane protein fhuE

C;Species: Escherichia coli

C;Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004

C;Accession: C64854; S09262; A26875; PC4409

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col

.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: C64854

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-729 <BLAT>

A;Cross-references: UNIPROT:P16869; GB:AE000210; GB:U00096; NID:g1787332; PIDN:AAAC74186.1

A;Experimental source: strain K-12, substrain MG1655

R;Sauer, M.; Hantke, K.; Braun, V.

Mol. Microbiol. 4, 427-437, 1990

A;Title: Sequence of the fhuE outer-membrane receptor gene of Escherichia coli K12 and p

A;Reference number: S09262; MUID:90286919; PMID:2162465

A;Accession: S09262

A;Molecule type: DNA

A;Residues: 1-362, 'C', 364-729 <SAU>

A;Cross-references: EMBL:X17615; NID:g41448; PIDN:CAA35616.1; PID:g41449

A;Experimental source: strain K-12

R;Sauer, M.; Hantke, K.; Braun, V.

J. Bacteriol. 169, 2044-2049, 1987

A;Title: Ferric-coprogen receptor FhuE of Escherichia coli: processing and sequence comm

A;Reference number: A26875; MUID:87194585; PMID:3032906

A;Accession: A26875

A;Molecule type: DNA

A;Residues: 1-69 <SA2>

R;Kobayashi, Y.; Sasanuma, A.; Nishimura, A.; Kuratomi, K.

Res. Commun. Biochem. Cell Mol. Biol. 1, 157-170, 1997

A;Title: A novel 14-kilodalton protein in P1,P4-bis(5'-adenosyl)tetrathosphate (Ap4A)-bir

A;Reference number: JC5685

A;Accession: PC4409

A;Molecule type: DNA

A;Residues: 1-47 <KOB>

C;Genetics:

A;Gene: fhuE

A;Map position: 16 min

C;Function:

A;Description: required for uptake of iron(III) via coprogen, ferrioxamine B and rhodotol C;Superfamily: ferrichrome-iron receptor; tonB-dependent receptor amino-terminal homolog C;Keywords: iron transport; membrane protein; receptor F;1-36/Domain: signal sequence #status predicted <SIG> F;37-729/Product: outer membrane protein fhuE #status predicted <MAT> F;97-230/Domain: tonB-dependent receptor amino-terminal homology <TNN> F;462-729/Domain: tonB-dependent receptor carboxyl-terminal homology <TNC>

Query Match 49.4%; Score 42; DB 2; Length 729;  
Best Local Similarity 42.9%; Pred. No. 70;  
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 SSDYSWMRKQNYVS 15  
|::|| | |::|  
Db 195 SAHYGSWNKERYVA 208

RESULT 6

H080813  
outer membrane receptor for ferric iron uptake ECs1480 [imported] - Escherichia coli (strain O157:H7)  
C;Species: Escherichia coli  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
C;Accession: H080813  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic reference number: A99629; MUID:21156231; PMID:11258796  
A;Reference number: A99629; MUID:21156231; PMID:11258796  
A;Accession: H080813  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-729 <HAY>  
A;Cross-references: UNIPROT:Q8X8H4; GB:BA0000007; PIDN:BA034903.1; PID:g133360944; GSPDB:G133360944  
A;Experimental source: strain O157:H7, substrain RMD 050952  
C;Genetics:  
A;Gene: ECs1480  
C;Superfamily: ferric-pseudobactin receptor; tonB-dependent receptor amino-terminal homolog

Query Match 49.4%; Score 42; DB 2; Length 729;  
Best Local Similarity 42.9%; Pred. No. 70;  
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 SSDYSWMRKQNYVS 15  
|::|| | |::|  
Db 195 SAHYGSWNKERYVA 208

RESULT 7

D85673  
outer membrane receptor for ferric iron uptake [imported] - Escherichia coli (strain O157:H7)  
C;Species: Escherichia coli  
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: D85673  
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, M.W.; Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Diallanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001  
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A;Reference number: A85480; MUID:21074935; PMID:11206551  
A;Accession: D85673  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-729 <STO>  
A;Cross-references: UNIPROT:Q8X8H4; GB:AB0001574; NID:g12514649; PIDN:AAG5848.1; GSPDB:G12514649  
A;Experimental source: strain O157:H7, substrain EDL933  
C;Genetics:  
A;Gene: fhuE  
C;Superfamily: ferric-pseudobactin receptor; tonB-dependent receptor amino-terminal homolog

Query Match 49.4%; Score 42; DB 2; Length 729;  
Best Local Similarity 42.9%; Pred. No. 70;  
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 SSDYSWMRKQNYVS 15

the amino-terminal region of this protein, appear to be required for the development of C:Genetics:

C:Gene: srfAB; srfA2  
C:Superfamily: surfactin synthetase; acetate-CoA ligase homology; acyl carrier protein h  
C:Keywords: antibiotic biosynthesis; carrier protein; duplication; ligase; phosphopantet  
F:511-951/Domain: acetate-CoA ligase homology <ACLI1>  
F:968-1035/Domain: acyl carrier protein homology <ACP1>  
F:1036-1481/Domain: repeat <RP11>  
F:1542-1995/Domain: acetate-CoA ligase homology <ACLI2>  
F:2013-2081/Domain: acetate-CoA ligase homology <ACLI2>  
F:2082-2529/Domain: repeat <RP2>  
F:2591-3024/Domain: acetate-CoA ligase homology <ACLI3>  
F:3041-3108/Domain: acyl carrier protein homology <ACP3>  
F:999,2045,3073/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

Query Match 49.4%; Score 42; DB 2; Length 3587;  
Best Local Similarity 50.0%; Pred. No. 3.4e+02;  
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 HSSDYSMRKNQ 12  
Db 1213 HYKDYAVWHKEQ 1224

RESULT 11  
E97103  
hypothetical protein CAC1650 [imported] - Clostridium acetobutylicum  
C:Species: Clostridium acetobutylicum  
C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
C:Accession: E97103  
F:Nalling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: E97103  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-121 <KUR>  
A:Cross-references: UNIPROT:Q971J1; GB:AE001437; PIDN:BAK79616.1; PID:G15024609; GSPDB:G  
A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CAC1650

Query Match 48.2%; Score 41; DB 2; Length 121;  
Best Local Similarity 58.3%; Pred. No. 17;  
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 DYSMRKNQYVS 15  
Db 19 DIITWKNQYVS 30

RESULT 12  
D82189  
conserved hypothetical protein VC1534 [imported] - Vibrio cholerae (strain N16961 serogr  
C:Species: Vibrio cholerae  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C:Accession: D82189  
F:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
F:1542-1995/Domain: Ermolava, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.  
1. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A:Reference number: A82035; MUID:20406833; PMID:10952301  
A:Accession: D82189  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-304 <HEI>  
A:Cross-references: UNIPROT:Q9KKV0; GB:AE004231; GB:AE003852; NID:G9656027; PIDN:AAF9468  
A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
C:Genetics:  
A:Gene: VC1534

A:Map position: 1

Query Match 48.2%; Score 41; DB 2; Length 304;  
Best Local Similarity 72.7%; Pred. No. 42;  
Matches 8; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

Qy 1 HSSDYSWVRKN 11  
| | | | |  
Db 8 HGSDY--WRKN 16

#### RESULT 13

G89921  
alanine dehydrogenase [imported] - Staphylococcus aureus (strain N315)  
C:Species: Staphylococcus aureus  
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C;Accession: G89921  
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc  
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;  
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
Lancet 357, 1225-1240, 2001  
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.  
A;Reference number: A89758; MUID:21311952; PMID:11418146  
A;Accession: G89921  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-372 <KUR>  
A;Cross-references: UNIPROT:Q9U049; GB:BA000018; PID:g13701237; PIDN:BA842532.1; GSPDB:G  
A;Experimental source: strain N315  
C;Genetics:  
A;Gene: SA1272  
C;Superfamily: alanine dehydrogenase; alanine dehydrogenase homology

Query Match 48.2%; Score 41; DB 2; Length 372;  
Best Local Similarity 42.9%; Pred. No. 52;  
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 HSSDYSWVRKNQYV 14  
| | | | | : | | : | |  
Db 76 HESEYQYFKKNQII 89

#### RESULT 14

S77661  
hypothetical protein o410 - Mycobacterium leprae  
C:Species: Mycobacterium leprae  
C;Date: 11-Oct-1997 #sequence\_revision 24-Oct-1997 #text\_change 09-Jul-2004  
C;Accession: S77661; S49524  
R;Psithi, H.; Cole, S.T.  
Mol. Microbiol. 16, 909-919, 1995  
A;Title: The Mycobacterium leprae genome: systematic sequence analysis identifies key ca  
A;Reference number: S77652; MUID:96059637; PMID:7476188  
A;Accession: S77661  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-410 <FSI>  
A;Cross-references: UNIPROT:Q50178; EMBL:246257; NID:G559905; PIDN:CAA86366.1; PID:G5599  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1994

Query Match 48.2%; Score 41; DB 2; Length 410;  
Best Local Similarity 46.7%; Pred. No. 57;  
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 HSSDYSWVRKNQYVS 15  
| | | | | : | | : | |  
Db 313 HSSDPNLWHRKFHAS 327

#### RESULT 15

G90268  
conserved hypothetical protein [imported] - Sulfolobus solfataricus  
C:Species: Sulfolobus solfataricus  
C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004

C;Accession: G90268  
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-y  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.  
arrett, R.A.; Ragan, M.A.; SENSEN, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A;Description: Sulfolobus solfataricus complete genome.  
A;Reference number: A99139  
A;Accession: G90268  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-432 <KUR>  
A;Cross-references: UNIPROT:Q97YZ4; GB:AE006641; NID:gl3814346; PIDN:AAK41406.1; GSPDB:G  
C;Genetics:  
A;Gene: SS01155

Query Match 48.2%; Score 41; DB 2; Length 432;  
Best Local Similarity 54.5%; Pred. No. 60;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 DYSWVRKNQYV 14  
| | | | | : | | : | |  
Db 12 DWNFWYKKNQYV 22

Search completed: June 3, 2005, 08:29:33  
Job time : 5 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 3, 2005, 07:50:56 ; Search time 14.1 Seconds  
(without alignments)

544.765 Million cell updates/sec

Title: US-10-616-279-10

Perfect score: 85

Sequence: 1 HSSDYSWVRKQVYS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	85	100.0	331	1	SPO2_HUMAN	Q8bdc6 homo sapien
2	82	96.5	289	2	Q6KAS6	Q8kas6 mus musculu
3	82	96.5	330	1	SPO2_MOUSE	Q8bme2 mus musculu
4	82	96.5	330	1	SPO2_RAT	Q8wv75 rattus norv
5	82	96.5	330	2	Q8VD28	Q8vdc2 mus musculu
6	63	74.1	331	2	Q42112	Q42112 brachydanio
7	55	64.7	313	2	Q6DCM4	Q6dcm4 xenopus lae
8	49	57.6	138	2	Q82UD3	Q82ud3 nitrosomona
9	49	57.6	420	2	Q22019	Q22019 cyanidiosch
10	49	57.6	446	2	Q85G84	Q85g84 cyanidiosch
11	47	55.3	390	2	Q7Y4U7	Q7y4u7 bacterioph
12	46	54.1	438	1	AMY1_HORVU	P00693 hordeum vul
13	46	54.1	438	2	Q40017	Q40017 hordeum vul
14	46	54.1	1453	2	Q755D1	Q755d1 ashbya goss
15	45	52.9	845	2	Q9GR11	Q9gr11 leishmania
16	44	51.8	434	2	Q81699	Q81699 avena fatua
17	44	51.8	434	2	Q87CW9	Q87cw9 xylella fas
18	44	51.8	437	2	Q81700	Q81700 avena fatua
19	44	51.8	839	2	Q8ML26	Q8ml26 drosophila
20	44	51.8	3099	2	Q7R514	Q7r514 giardia lam
21	43.5	51.2	545	1	SRB4_SCHPO	P87306 schizosacch
22	43.5	51.2	570	2	Q8D4R4	Q8d4r4 vibrio vuln
23	43.5	51.2	602	2	Q7MG88	Q7mg88 vibrio vuln
24	43	50.6	273	1	HIS6_METAC	Q8tt96 methanosarc
25	43	50.6	463	2	Q89K98	Q89kw8 bradyrhizob
26	43	50.6	809	2	Q7NAF2	Q7naf2 mycoplasma
27	42	49.4	92	2	Q6DC15	Q6dc15 brachydanio
28	42	49.4	105	2	Q73915	Q73915 bacillus ce
29	42	49.4	206	2	Q99L35	Q99l35 mus musculu
30	42	49.4	230	2	Q7T5M1	Q7t5m1 cryptocophle
31	42	49.4	239	2	Q8JR20	Q8jr20 phthorimaea

32	42	49.4	294	1	TNE7_HUMAN	O98588 homo sapien
33	42	49.4	294	2	Q6UM79	O6uw79 homo sapien
34	42	49.4	422	2	Q6YQK6	Q6yqk6 onion yello
35	42	49.4	435	1	AM3D_ORYSA	P27933 oryza sativ
36	42	49.4	436	2	Q6ZDD5	Q6zdd5 oryza sativ
37	42	49.4	442	2	Q7SDN5	Q7sdn5 neurospora
38	42	49.4	504	2	Q6L0Z8	Q6l0z8 picophilus
39	42	49.4	729	1	PHUE_ECOLI	P16869 escherichia
40	42	49.4	729	2	Q7AF82	Q7af82 escherichia
41	42	49.4	729	2	Q8X8H4	Q8x8h4 escherichia
42	42	49.4	729	2	Q8CW53	Q8cw53 escherichia
43	42	49.4	734	2	Q69DL2	Q69dl2 sus scrofa
44	42	49.4	877	2	Q06593	Q06593 saccharomyc
45	42	49.4	1080	2	O84688	O84688 chlamydia t

#### ALIGNMENTS

RESULT 1  
ID SPO2\_HUMAN STANDARD; PRT; 331 AA.  
AC Q8BUD6; Q9ULW1;  
DT 25-OCT-2004 (Rel. 45, Created)  
DT 25-OCT-2004 (Rel. 45, Last sequence update)  
DT 25-JAN-2005 (Rel. 46, Last annotation update)  
DE Spondin 2 precursor (Mindin) (Differentially expressed in cancerous  
DE and noncancerous lung cells 1) (DIL-1) (UNQ495/PRO866).  
GN Name=SPON2; Synonyms=DIL1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RN  
RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND VARIANTS ALA-122 AND  
VAL-242.  
RX MEDLINE=99443867; PubMed=10512675; DOI=10.1006/geno.1999.5939;  
RA Manda K., Kohno T., Matsuno Y., Takenoshita S., Kuwano H., Yokota J.;  
RT "Identification of genes (SPON2 and C20orf2) differentially expressed  
RT between cancerous and noncancerous lung cells by mRNA differential  
RT display.";  
RL Genomics 61:5-14(1999).  
[2]  
RN  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,  
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
RA Godowski P., Gray A.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
RT effort to identify novel human secreted and transmembrane proteins: a  
RT bioinformatics assessment.";  
RL Genome Res. 13:2265-2270(2003).  
[3]  
RN  
RP SEQUENCE FROM N.A. AND VARIANTS ALA-122 AND VAL-242.  
RX PubMed=14702039; DOI=10.1038/ng1285;  
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,  
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,  
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,  
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,  
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,  
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,  
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,  
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,  
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoaka S., Chiba Y.,  
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,  
RA Kusano S., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,

RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,  
RA Inose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,  
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,  
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,  
RA Yamazaki M., Watanabe K., Kunagai A., Itakura S., Fukuzumi Y.,  
RA Fujimori Y., Koniya M., Tashiro H., Tanigami A., Fujiwara T.,  
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hixao M., Ohmori Y.,  
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
RA Togauchi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,  
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isoqai T., Sugano S.,  
RT "Complete sequencing and characterization of 21,243 full-length human  
RT cDNAs.";  
RL Nat. Genet. 36:40-45(2004).  
RN [4]  
RN SEQUENCE FROM N.A.  
RC TISSUE=Colon, and Placenta;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villallon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).  
CC -1- FUNCTION: Cell adhesion protein that promote adhesion and  
CC outgrowth of hippocampal embryonic neurons. Binds directly to  
CC bacteria and their components and functions as an opsonin for  
CC macrophage phagocytosis of bacteria. Essential in the initiation  
CC of the innate immune response and represents a unique pattern-  
CC recognition molecule in the ECM for microbial pathogens (By  
CC similarity).  
CC -1- SUBCELLULAR LOCATION: Secreted. Extracellular matrix (By  
CC similarity).  
CC -1- TISSUE SPECIFICITY: Expressed in normal lung tissues but not in  
CC lung carcinoma cell lines.  
CC -1- SIMILARITY: Contains 1 spondin domain.  
CC -1- SIMILARITY: Contains 1 TSP type-1 domain.  
CC -----  
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CC -----  
CC ENBL; AB027466; BAA85892.1; -  
CC ENBL; AY358948; AAQ89307.1; -  
CC ENBL; AK074618; BAC11092.1; -  
CC ENBL; AK074770; BAC11196.1; -  
CC ENBL; BC002707; AAC02707.1; -  
CC ENBL; BC036341; AAH36341.1; -  
CC Genew; HGNC:11253; SPON2.  
CC H-InvDB; HIX0004013; -.

DR MTM; 605918; -.  
DR InterPro; IPR009465; Spond\_N.  
DR InterPro; IPR000884; TSP1.  
DR Pfam; PF06468; Spond\_N; 1.  
DR Pfam; PF00090; TSP\_1; 1.  
DR PROSITE; PS1020; SPONDIN; 1.  
DR PROSITE; PS50092; TSP1; 1.  
KW Cell adhesion; Extracellular matrix; Immune response; Polymorphism;  
KW Signal.  
FT SIGNAL 1 26 Potential.  
FT CHAIN 27 331 Spondin 2.  
FT DOMAIN 31 221 Spondin.  
FT DOMAIN 277 331 TSP type-1.  
FT VARIANT 40 40 P -> L (in dbSNP:922697).  
FT VARIANT 122 122 /FTID=VAR\_019701.  
FT VARIANT 242 242 E -> A (in dbSNP:11247975).  
FT VARIANT 242 242 /FTID=VAR\_019702.  
FT VARIANT 242 242 /FTID=VAR\_019703.  
FT VARIANT 242 242 L -> V (in dbSNP:2279279).  
SQ SEQUENCE 331 AA; 35844 MW; 418E244B893C59F4 CRC64;  
Query Match 100.0%; Score 85; DB 1; Length 331;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05; Indels 0; Gaps 0;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HSSDYSWMRKQYVS 15  
DB 77 HSSDYSWMRKQYVS 91  
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RESULT 2  
Q6KAS6 PRELIMINARY; PRT; 289 AA.  
ID Q6KAS6 PRELIMINARY; PRT; 289 AA.  
AC Q6KAS6;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE MFLJ00108 protein (Fragment).  
GN Names=MFLJ00108;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,  
RA Saga Y., Kitamura H., Nakagawa T., Nagase T., Ohara O., Koga H.;  
RT "Prediction of the Coding Sequences of Mouse Homologues of FLJ Genes:  
RT The Complete Nucleotide Sequences of 110 Mouse FLJ-Homologous cDNAs  
RT Identified by Screening of Terminal Sequences of cDNA Clones Randomly  
RT Sampled from Size-Fractionated Libraries.";  
RL DNA Res. 11:167-180(2004).  
DR ENBL; AK131131; BAD21381.1; -  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR InterPro; IPR009465; Spond\_N.  
DR InterPro; IPR000884; TSP1.  
DR Pfam; PF06468; Spond\_N; 1.  
DR Pfam; PF00090; TSP\_1; 1.  
DR SMART; SM00209; TSP1; 1.  
DR PROSITE; PS50092; TSP1; 1.  
FT NON\_TER 1 1  
SQ SEQUENCE 289 AA; 31664 MW; 7FECE944C03021E9 CRC64;  
Query Match 96.5%; Score 82; DB 2; Length 289;  
Best Local Similarity 93.3%; Pred. No. 3.3e-05; Indels 0; Gaps 0;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HSSDYSWMRKQYVS 15  
DB 35 HSSDYSWMRKQYVS 49  
|||||  
RESULT 3



SP02\_MOUSE  
ID SP02\_MOUSE STANDARD; PRT; 330 AA.  
AC QBMS2; QesJDB;  
DT 25-OCT-2004 (Rel. 45, Created)  
DT 25-OCT-2004 (Rel. 45, Last sequence update)  
DE 25-JAN-2005 (Rel. 46, Last annotation update)  
DE Spondin 2 precursor (Mindin).  
GN Name=Spon2;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A., AND FUNCTION.  
RC TISSUE=Thymus;  
RX PubMed=14691481; DOI=10.1038/nr1021;  
RA He Y.-W., Li H., Zhang J., Hsu C.-L., Lin E., Zhang N., Guo J.,  
RA Forbush K.A., Bevan M.J.;  
RT "The extracellular matrix protein mindin is a pattern-recognition  
RT molecule for microbial pathogens";  
RL Nat. Immunol. 5:88-97(2004).  
RN [2]  
RN SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Skin;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gofjohori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Macleoda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Glasi C., Godzik A., Gough J.,  
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numa K., Okido T., Pavan W.J., Perlea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tonita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yangisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RL Nature 420:563-573 (2002).  
RL Nature 420:563-573 (2002).  
CC -1- FUNCTION: Cell adhesion protein that promote adhesion and  
CC outgrowth of hippocampal embryonic neurons. Binds directly to  
CC bacteria and their components and functions as an opsonin for  
CC macrophage phagocytosis of bacteria. Essential in the initiation  
CC of the innate immune response and represents a unique pattern-  
CC recognition molecule in the ECM for microbial pathogens.  
CC -1- SUBCELLULAR LOCATION: Secreted. Extracellular matrix.  
CC -1- SIMILARITY: Contains 1 spondin domain.  
CC -1- SIMILARITY: Contains 1 TSP type-1 domain.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; AK028987; BAC26226.1; -

EMBL; AY457639; AAR20834.1; -  
MGD; MGI:1923724; Spon2.  
InterPro; IPR009465; Spond\_N.  
InterPro; IPR00884; TSP1.  
Pfam; PF06468; Spond\_N; 1.  
Pfam; PF00090; TSP\_1; 1.  
SMART; SM00209; TSP1; 1.  
PROSITE; PS1020; SPONDIN; 1.  
PROSITE; PS00092; TSP1; 1.  
Cell adhesion; Extracellular matrix; Immune response; Signal.  
Potential.  
Spondin 2.  
FT CHAIN 1 25  
FT DOMAIN 26 330  
FT DOMAIN 30 220  
FT DOMAIN 276 330  
FT CONFLICT 242 242  
FT CONFLICT R -> Q (in Ref. 2).  
SQ SEQUENCE 330 AA; 35964 MW; 581F16B6A55F9A07 CRC64;  
Query Match 96.5%; Score 82; DB 1; Length 330;  
Best Local Similarity 93.3%; Pred. No. 3.8e-05;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HSSDYSNWRKNQYVS 15  
DB 76 HSSDYSNWRKNQYVS 90  
|||||  
RESULT 4  
SP02\_RAT  
ID SP02\_RAT STANDARD; PRT; 330 AA.  
AC Q9WV75;  
DT 25-OCT-2004 (Rel. 45, Created)  
DT 25-OCT-2004 (Rel. 45, Last sequence update)  
DT 25-JAN-2005 (Rel. 46, Last annotation update)  
DE Spondin 2 precursor (Mindin).  
GN Name=Spon2;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RN SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.  
RC STRAIN=Sprague-Dawley;  
RX MEDLINE=9933991; PubMed=10409509;  
RA Feinstein Y., Borrell V., Garcia C., Burstyn-Cohen T., Tzarfaty V.,  
RA Frumkin A., Nose A., Okamoto H., Higashijima S., Soriano A., Klar A.;  
RA "F-spondin and mindin: two structurally and functionally related genes  
RA expressed in the hippocampus that promote outgrowth of embryonic  
RA hippocampal neurons";  
RL Development 126:3637-3648(1999).  
RN [2]  
RN SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RG NIH - Mammalian Gene Collection (MGC) project;  
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Cell adhesion protein that promote adhesion and  
CC outgrowth of hippocampal embryonic neurons. Binds directly to  
CC bacteria and their components and functions as an opsonin for  
CC macrophage phagocytosis of bacteria. Essential in the initiation  
CC of the innate immune response and represents a unique pattern-  
CC recognition molecule in the ECM for microbial pathogens (By  
CC similarity).  
CC -1- SUBCELLULAR LOCATION: Secreted. Extracellular matrix.  
CC -1- TISSUE SPECIFICITY: Abundantly expressed in the developing  
CC hippocampus.  
CC -1- SIMILARITY: Contains 1 spondin domain.  
CC -1- SIMILARITY: Contains 1 TSP type-1 domain.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; AK028987; BAC26226.1; -

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CQ		
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RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.;  
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
RT initiative";  
RL Dev. Dyn. 225:384-391(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Embryo;  
RC PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Joquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villallon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalish A., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Embryo;  
RC Klein S., Gerhard D.S.;  
RL Submitted (JUL-2004) to the ENBL/GenBank/DBSJ databases.  
DR EMBL; BC077984; AAH7984.1; -;  
DR GO; GO:0007155; P:cell adhesion; IEA.  
DR GO; GO:0007275; P:development; IEA.  
DR InterPro; IPR009465; Spod\_N.  
DR InterPro; IPR000884; TSP1\_N.  
DR Pfam; PF06468; Spod\_N; 1.  
DR Pfam; PF00090; TSP1; 1.  
DR SMART; SM00209; TSP1; 1.  
DR PROSITE; PS00092; TSP1; 1.  
SQ SEQUENCE 313 AA; 34476 MW; 686F610A18ED28E9 CRC64;  
Query Match 64.7%; Score 55; DB 2; Length 313;  
Best Local Similarity 66.7%; Pred. No. 0.93;  
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 HSSDYSWMRKNOYVS 15  
Db 61 HSSDYHMKLEPVS 75  
|||||:|:|:|:|  
|||:|:|:|:|  
RESULT 8  
Q82UD3 PRELIMINARY; PRT; 138 AA.  
AC Q82UD3;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein.  
GN OrderedLocNames=NE1559;  
OS Nitrosomonas europaea.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;  
OC Nitrosomonadaceae; Nitrosomonas.  
OX NCBI\_TaxID=915;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 19718 / IFO 14298;

RX MEDLINE=22586410; PubMed=12700255;  
RX Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.L.,  
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,  
RA Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;  
RT "Complete genome sequence of the ammonia-oxidizing bacterium and  
RT obligate chemolithoautotroph Nitrosomonas europaea";  
RL J. Bacteriol. 185:2759-2773(2003).  
DR EMBL; BX321861; CAD85470.1; -;  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 138 AA; 15572 MW; 54326051C08B07C6 CRC64;  
Query Match 57.6%; Score 49; DB 2; Length 138;  
Best Local Similarity 57.1%; Pred. No. 3.7;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 HSSDYSWMRKNOYV 14  
Db 39 HASDQSLMSDTQIV 52  
|||||:|:|:|:|  
|||:|:|:|:|  
RESULT 9  
O22019 PRELIMINARY; PRT; 420 AA.  
AC O22019;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE ORF420.  
OS Cyanidioschyzon merolae (Red alga).  
OC Eukaryota; Rhodophyta; Bangiophyceae; Cyanidiales; Cyanidiaceae;  
OC Cyanidioschyzon.  
OX NCBI\_TaxID=45157;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ohta N.;  
RT "Analysis of a plastid gene cluster reveals a close relationship  
RT between Cyanidioschyzon and Cyanidium";  
RL J. Plant Res. 110:235-245(1997).  
DR EMBL; D63675; BAA22815.1; -;  
DR GO; GO:0005525; F:GTP binding; IEA.  
DR GO; GO:0003743; F:translation initiation factor activity; IEA.  
DR GO; GO:0006413; P:translational initiation; IEA.  
DR InterPro; IPR000178; IF2.  
DR InterPro; IPR006847; IF2\_N.  
DR InterPro; IPR009000; Translat\_factor.  
DR Pfam; PF04760; IF2\_N; 1.  
DR ProDom; PD186100; IF2; 1.  
SQ SEQUENCE 420 AA; 47691 MW; A6CAE107B24B4E19 CRC64;  
Query Match 57.6%; Score 49; DB 2; Length 420;  
Best Local Similarity 70.0%; Pred. No. 12;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Qy 4 DYSWMRKNOY 13  
Db 366 EYEIWRKNOY 375  
|||||:|:|:|:|  
|||:|:|:|:|  
RESULT 10  
Q85G84 PRELIMINARY; PRT; 446 AA.  
AC Q85G84;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Initiation factor 2.  
GN Name=infB;  
OS Cyanidioschyzon merolae (Red alga).  
OC Chloroplast.  
OC Eukaryota; Rhodophyta; Bangiophyceae; Cyanidiales; Cyanidiaceae;  
OC Cyanidioschyzon.  
OX NCBI\_TaxID=45157;

RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=100;  
RX MEDLINE=22639682; PubMed=12755171;  
RA Ohta N., Matsuaki M., Misumi O., Miyagishima S., Nozaki H.,  
Tanaka K., Shin-i T., Kohara Y., Kuroiwa T.;  
RT "Complete Sequence and Analysis of the Plastid Genome of the  
RT Unicellular Red Alga Cyanidioschyzon merolae.";  
RL DNA Res. 10:67-77(2003).  
DR EMBL: AB002583; BAC76102.1; -.  
DR GO: GO:0009507; C:chloroplast; IEA.  
DR GO: GO:0005225; F:GTP binding; IEA.  
DR GO: GO:0003743; F:translation initiation factor activity; IEA.  
DR GO: GO:0006413; P:translational initiation; IEA.  
DR InterPro: IPR00178; IPF2.  
DR InterPro: IPR006847; IPF2\_N.  
DR InterPro: IPR009000; Translat\_factor.  
DR Pfam: PF04760; IPF2\_N; 1.  
DR ProDom: PD186100; IPF2; 1.  
KW Chloroplast; Initiation factor.  
SQ SEQUENCE 446 AA; 50850 MW; 89A8BD5483020527 CRC64;

Query Match 57.6%; Score 49; DB 2; Length 446;  
Best Local Similarity 70.0%; Pred. No. 13;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 DYSWKRKNQY 13  
:|:|||||  
Db 392 EYEWKRKNQY 401

RESULT 11  
QY4U7 PRELIMINARY; PRT; 390 AA.  
AC QY4U7;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE G27 baseplate hub subunit.  
OS Bacteriophage RB69.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;  
OC T4-like viruses.  
OX NCBI\_TaxID=12353;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98215164; PubMed=9555879;  
RA Yeh L.S., Hsu T., Karam J.D.;  
RT "Divergence of a DNA replication gene cluster in the T4-related  
RT bacteriophage RB69.";  
RL J. Bacteriol. 180:2005-2013(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20566703; PubMed=11114936; DOI=10.1128/JB.183.1.358-366.2001;  
RA Tetart F., Desplats C., Kutateladze M., Monod C., Ackermann H.W.,  
RA Krisch H.M.;  
RT "Phylogeny of the major head and tail genes of the wide-ranging T4-  
RT type bacteriophages.";  
RL J. Bacteriol. 183:358-366(2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96064739; PubMed=7592876; DOI=10.1074/jbc.270.44.26558;  
RA Wang C.C., Yeh L.S., Karam J.D.;  
RT "Modular organization of T4 DNA polymerase. Evidence from  
RT phylogenetics.";  
RL J. Biol. Chem. 270:26558-26564(1995).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97358535; PubMed=9215631; DOI=10.1016/S0092-8674(00)80296-2;  
RA Wang J., Sattar A.K., Wang C.C., Karam J.D., Konigsberg W.H.,  
RA Steitz T.A.;  
RT "Crystal structure of a pol alpha family replication DNA polymerase  
RT from bacteriophage RB69.";  
RL Cell 89:1087-1099(1997).

RN [5]  
RP SEQUENCE FROM N.A.  
RA Borjac J., Petrov V.M., Karam J.D.;  
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RA Petrov V., Nolan J., Chin D., Letarov A., Krisch H.M., Karam J.D.;  
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY303349; AAF76103.1; -.  
SQ SEQUENCE 390 AA; 44285 MW; C0523000DD657817 CRC64;  
  
Query Match 55.3%; Score 47; DB 2; Length 390;  
Best Local Similarity 63.6%; Pred. No. 24;  
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 DYSWKRKNQY 14  
|||||:|:|:  
Db 19 DYSWQENRYV 29  
  
RESULT 12  
AMYL HORVU STANDARD; PRT; 438 AA.  
ID AMYL\_HORVU  
AC P00693;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Alpha-amylase type A isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-  
DE Glucan glucanohydrolase) (AMYL) (Low pI alpha-amylase).  
GN Name=AMYL.1;  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Hordeum.  
OX NCBI\_TaxID=4513;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Himalaya;  
RX MEDLINE=83238423; PubMed=6190808;  
RA Rogers J.C., Millman C.;  
RT "Isolation and sequence analysis of a barley alpha-amylase cDNA  
RT clone.";  
RL J. Biol. Chem. 258:8169-8174(1983).  
RN [2]  
RP MUTAGENESIS OF HIS-117; ASP-204; GLU-229; TRP-303; HIS-314 AND  
RP ASP-315  
RX PubMed=7901200;  
RA Sogaard M., Kadziola A., Haer R., Svensson B.;  
RT "Site-directed mutagenesis of histidine 93, aspartic acid 180,  
RT glutamic acid 205, histidine 290, and aspartic acid 291 at the active  
RT site and tryptophan 279 at the raw starch binding site in barley  
RT alpha-amylase 1.";  
RL J. Biol. Chem. 268:22480-22484(1993).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 25-428.  
RX PubMed=12906828;  
RA Robert X., Haer R., Gottschalk T.E., Ratajczak P., Driguez H.,  
RA Svensson B., Aghajari N.;  
RT "The structure of barley alpha-amylase isozyme 1 reveals a novel role  
RT of domain C in substrate recognition and binding: a pair of sugar  
RT tongs.";  
RL Structure 11:973-984(2003).  
CC -I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic  
CC linkages in oligosaccharides and polysaccharides.  
CC -I- COFACTOR: Binds 3 calcium ions per subunit (By similarity).  
CC -I- SUBUNIT: Monomer (By similarity).  
CC -I- SUBCELLULAR LOCATION: Extracellular.  
CC -I- DEVELOPMENTAL STAGE: Production of alpha-amylase is hormonally  
CC regulated. Germinating embryos produce the hormone gibberellic  
CC acid, which within 10 hours stimulates the aleurone cells covering  
CC the endosperm of the seed to produce alpha-amylase. The enzyme  
CC then degrades the starch within the endosperm for use by the  
CC developing plant embryo.



KW Nuclear protein.  
SQ SEQUENCE 1453 AA; 164938 MW; ELC3DA8556FA406E CRC64;  
Query Match 54.1%; Score 46; DB 2; Length 1453;  
Best Local Similarity 54.5%; Pred. No. 1.4e+02;  
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HSDYSMWKKN 11  
|::|::|::|  
Db 990 HNASYAVWKN 1000

RESULT 15  
Q9GRL1 PRELIMINARY; PRT; 845 AA.  
AC Q9GRL1; 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein P214.31.  
GN Name=P214.31;  
OS Leishmania major.  
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
OX NCBI\_TaxID=5664;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Friedlin;  
RX MEDLINE=98146435; PubMed=9477341;  
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,  
RA Smith D.F.;  
RT "A physical map of the Leishmania major Friedlin genome.";  
RL Genome Res. 8:135-145(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Friedlin;  
RA Saunders D., Murphy L., Harris D., Ivens A.C., Quail M.,  
RA Rajandream M.A., Barrell B.G.;  
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL449144; CAC14638.1; -.  
DR InterPro; IPR000626; Ubiquitin.  
DR Pfam; PF00240; ubiquitin; 1.  
DR SMART; SM00213; UBQ; 1.  
DR PROSITE; PS50053; UBIQUITIN\_2; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 845 AA; 89557 MW; 57CA41EA2D94A5B2 CRC64;  
Query Match 52.9%; Score 45; DB 2; Length 845;  
Best Local Similarity 53.8%; Pred. No. 1.2e+02;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 HSDYSMWKKNQY 13  
|::|::|::|  
Db 826 HSGDWNWEANPY 838

Search completed: June 3, 2005, 08:28:08  
Job time : 16.1 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 3, 2005, 07:49:16 ; Search time 15.825 Seconds  
(without alignment)  
366.598 Million cell updates/sec

Title: US-10-616-279-10

Perfect score: 85

Sequence: 1 HSSDYSWRKNQIVS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	15	4 AAB82474	Aab82474 Human ext
2	85	100.0	290	2 AAW83329	Aaw83329 Human min
3	85	100.0	330	4 AAE12304	Aae12304 Human NPG
4	85	100.0	331	2 AAW23663	Aaw23663 Human neu
5	85	100.0	331	2 AAW70589	Aaw70589 Adhesion-
6	85	100.0	331	2 AAW83328	Aaw83328 Human min
7	85	100.0	331	2 AAY41721	Aay41721 Human PRO
8	85	100.0	331	2 AAW92460	Aaw92460 Human NAF
9	85	100.0	331	3 AAB33465	Aab33465 Human PRO
10	85	100.0	331	3 AAY79561	Aay79561 Cancer sp
11	85	100.0	331	3 AAB44277	Aab44277 Human PRO
12	85	100.0	331	3 AAY95349	Aay95349 Human PRO
13	85	100.0	331	4 AAW93266	Aaw93266 Human pol
14	85	100.0	331	4 AAM93324	Aam93324 Human pol
15	85	100.0	331	4 AAM38872	Aam38872 Human pol
16	85	100.0	331	4 AAB82472	Aab82472 Human ext
17	85	100.0	331	5 ABG61806	Abg61806 Prostate
18	85	100.0	331	5 AAU79944	Aau79944 Human Spo
19	85	100.0	331	5 AAB77393	Aab77393 Human spo
20	85	100.0	331	5 AAE20463	Aae20463 Human tum
21	85	100.0	331	6 ABO25223	AbO25223 Novel hum
22	85	100.0	331	6 ABU72229	Abu72229 Novel hum
23	85	100.0	331	6 ABU84909	Abu84909 Human sec
24	85	100.0	331	6 ABU61107	Abu61107 Human PRO
25	85	100.0	331	6 ABU80376	Abu80376 Human sec

## ALIGNMENTS

## RESULT 1

AAB82474

ID AAB82474 standard; peptide; 15 AA.

XX AC AAB82474;

XX DT 22-AUG-2001 (first entry)

XX DE Human extracellular matrix protein RGI immunogenic peptide 3C.

KW RGI; human; extracellular matrix protein; prostate cancer; metastasis;  
KW tumour; benign prostatic hyperplasia; therapy; diagnosis; antitumour;  
KW immunogen.

XX OS Homo sapiens.

XX PN WO200144291-A2.

XX PD 21-JUN-2001.

XX PF 15-DEC-2000; 2000WO-US033901.

XX PR 16-DEC-1999; 99US-0172370P.

XX PR 07-DEC-2000; 2000US-00732357.

XX (SCHD ) SCHERING AG.

XX Harkins R, Parkes D, Parry G, Schneider DW, Steinbrecher R;

XX WPI; 2001-398128/42.

XX Novel human extracellular matrix polypeptide, RGI, useful in research,  
XX diagnosis and treatment of metastasis such as prostate cancer.

XX Claim 26; Page 48; 69pp; English.

XX The present sequence is that of immunogenic peptide 3C of human RGI (see  
XX AAB82472). RGI is a new homologue of the extracellular matrix protein  
XX family that is expressed in prostate tissue and which may be over-  
XX expressed in prostate tumours. Peptide 3C corresponds to amino acid  
XX residues 77-91 of RGI. It was selected as a potential immunogen because  
XX of its predicted position at the surface of the protein. Antisera raised  
XX against peptide 3C recognise RGI. An antibody that specifically binds to  
XX the peptide is claimed. The invention provides human RGI polypeptides,  
XX polynucleotides encoding them, and antibodies which specifically bind RGI  
XX or a polypeptide such as the present sequence. Such antibodies can be  
XX used for diagnosis and/or detection of RGI expression, or can be  
XX conjugated (e.g. as an Fv, F(ab') or F(ab')<sub>2</sub> fragment) to a therapeutic

26 85 100.0 331 6 ABG75949 Abg75949 Human ant  
27 85 100.0 331 6 ADA24775 Ada24775 Novel hum  
28 85 100.0 331 6 ABO19678 Abo19678 Novel hum  
29 85 100.0 331 6 ADA12436 Ada12436 Human sec  
30 85 100.0 331 6 ABO19569 Abo19569 Novel hum  
31 85 100.0 331 7 ADB73742 Adb73742 Human PRO  
32 85 100.0 331 7 ADB76458 Adb76458 Human PRO  
33 85 100.0 331 7 ADB75561 Adb75561 Prostate  
34 85 100.0 331 7 ADC43884 Adc43884 Human sec  
35 85 100.0 331 7 ADC61644 Adc61644 Human sec  
36 85 100.0 331 7 ADC63608 Adc63608 Human sec  
37 85 100.0 331 7 ADC66708 Adc66708 Human sec  
38 85 100.0 331 7 ADC68832 Adc68832 Human sec  
39 85 100.0 331 7 ADC82892 Adc82892 Human sec  
40 85 100.0 331 7 ADC67957 Adc67957 Human sec  
41 85 100.0 331 7 ADC41277 Adc41277 Human sec  
42 85 100.0 331 7 ADC67332 Adc67332 Human sec  
43 85 100.0 331 7 ADC62268 Adc62268 Human sec  
44 85 100.0 331 7 ADC41901 Adc41901 Human sec  
45 85 100.0 331 7 ADE49270 Ade49270 Human sec

CC agent, especially a cytotoxic agent, for administration to a patient for  
 CC treatment of diseases characterised by Rgl activity or expression, such  
 CC as prostate cancer

SQ Sequence 15 AA;  
 Query Match 100.0%; Score 85; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HSSDYSWVRKNQYVS 15  
 |||||  
 Db 1 HSSDYSWVRKNQYVS 15

RESULT 2  
 AAW83329  
 ID AAW83329 standard; protein; 290 AA.  
 XX AC AAW83329;  
 XX DT 01-MAR-1999 (first entry)  
 XX DE Human mindin-related polypeptide.  
 XX Mindin; human; integrin ligand; angiogenic disease; cancer; metastasis;  
 KW chronic inflammatory disorder; rheumatoid arthritis; atherosclerosis;  
 KW macular degeneration, diabetic retinopathy; restenosis;  
 KW Alzheimer's disease; neural disorder; tissue remodelling; therapy;  
 KW diagnosis.  
 XX OS Homo sapiens.  
 XX PN WO9850073-A1.  
 XX PD 12-NOV-1998.  
 XX PF 07-MAY-1998; 98WO-US009476.  
 XX PR 09-MAY-1997; 97US-0046106P.  
 XX PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX PI Jonak ZL, Trulli SH, Tsui P, Lane PA;  
 XX WPI: 1999-034688/03.  
 XX N-PSDB; AAV72538.

PT A new polypeptide is the integrin ligand, human mindin - useful in  
 PT therapy and diagnostic assays for diseases such as those associated with  
 PT angiogenesis.

PS Claim 14; Page 30-31; 39pp; English.

CC This amino acid sequence was deduced from the nucleotide sequence (see  
 CC AAV72538) of expressed sequence tags identified prior to the isolation of  
 CC a full-length sequence (see AAV72537) encoding human mindin (see  
 CC AAW83328). Claimed polypeptides have an amino acid sequence which has at  
 CC least 70%, 80%, 90%, 95% or 97-77% identity to this polypeptide, or  
 CC comprise the amino acid sequence of the polypeptide itself, or are  
 CC encoded by a polynucleotide comprising the sequence contained in  
 CC AAV72538. The invention relates to human mindin polypeptides and  
 CC polynucleotides (see also AAV72537). Mindin is a novel integrin ligand  
 CC suggested to have multifunctional activity in normal and disease states.  
 CC Methods are provided for using mindin polypeptides and polynucleotides in  
 CC the treatment and diagnosis of angiogenic diseases (cancer, cancer  
 CC metastasis, chronic inflammatory disorders, rheumatoid arthritis,  
 CC atherosclerosis, macular degeneration, diabetic retinopathy), restenosis,  
 CC Alzheimer's disease, neural disorders and tissue remodelling. The  
 CC invention also relates to methods for identifying agonists and  
 CC antagonists/inhibitors and for treating conditions associated with human  
 CC mindin imbalance with the identified compounds. Diagnostic assays for  
 CC detecting diseases associated with inappropriate human mindin activity or

CC levels are also claimed  
 XX Sequence 290 AA;  
 SQ

Query Match 100.0%; Score 85; DB 2; Length 290;  
 Best Local Similarity 100.0%; Pred. No. 9.1e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HSSDYSWVRKNQYVS 15  
 |||||  
 Db 77 HSSDYSWVRKNQYVS 91

RESULT 3  
 AAE12304  
 ID AAE12304 standard; protein; 330 AA.  
 XX AC AAE12304;  
 XX DT 03-JAN-2002 (first entry)  
 XX DE Human NPG-1 protein.  
 XX Human; NPG-1; cytostatic; gene therapy; tumour; prostrate cancer; LCS;  
 KW Linker Capture Subtraction; genetic alteration; nerve cell growth.  
 XX OS Homo sapiens.  
 XX PN US6287777-B1.  
 XX PD 11-SEP-2001.  
 XX PF 10-AUG-1999; 99US-00371696.  
 XX PR 10-MAY-1996; 96US-00644326.  
 XX PD 11-FEB-1998; 98US-00022238.  
 XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
 XX Sytkowski AJ, Yang M;  
 XX WPI: 2001-624488/72.  
 XX N-PSDB; AAD20094.

PT Detecting the presence of a nucleic acid encoding NPG-1 in a sample  
 PT comprises contacting the sample with a nucleic acid probe or primer which  
 PT hybridizes under stringent conditions to NPG-1 nucleic acid.

XX Example; Fig 2; 35pp; English.

CC The invention relates to a method termed Linker Capture Subtraction (LCS)  
 CC for detecting the presence of a nucleic acid encoding NPG-1. NPG-1 gene  
 CC is differentially expressed in prostrate tumours. The method is used for  
 CC identifying nucleic acids encoding NPG-1. NPG-1 can be used for treating  
 CC a subject having a tumour, cancer, for the adhesion and outgrowth of  
 CC axon, for stimulating growth of nerve cell, and regenerating nerve cells.  
 CC The NPG-1 nucleic acids, protein and antibodies may be used in screening  
 CC assays, detecting assays, and predictive medicine. The nucleic acids are  
 CC further used to express an NPG-1 protein, to detect NPG-1 mRNA or a  
 CC genetic alteration in an NPG-1 gene, and to modulate NPG-1 activity. The  
 CC present sequence is human NPG-1 protein

XX Sequence 330 AA;

Query Match 100.0%; Score 85; DB 4; Length 330;  
 Best Local Similarity 100.0%; Pred. No. 1e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HSSDYSWVRKNQYVS 15  
 |||||  
 Db 77 HSSDYSWVRKNQYVS 91



```

RESULT 4
AAW23663
ID AAW23663 standard; protein; 331 AA.
XX
XX AC AAW23663;
XX
XX DT 08-MAR-1998 (first entry)
XX
XX DE Human neuronal attachment factor-1.
XX
XX KW Neuronal attachment factor-1; NAF-1; human; cell-cell interaction;
XX cell adhesion; spinal cord injury; peripheral nerve damage; tumour;
XX KW metastasis; therapy; malaria; wound healing.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX Peptide 1..23
XX FT /label= Sig_peptide
XX FT 24..331
XX FT /label= Mat_protein
XX
XX PN WO9729189-A1.
XX
XX PD 14-AUG-1997.
XX
XX PF 12-FEB-1996; 96WO-US001857.
XX
XX PR 12-FEB-1996; 96WO-US001857.
XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Hastings GA;
XX
XX DR WPI: 1997-415344/38.
XX DR N-PSDB; AAT78360.
XX
XX PT New isolated human neuronal attachment factor-1 - promotes cell-cell
XX interaction and cell adhesion, used for treating e.g. spinal cord injury,
XX peripheral nerve damage or tumours.
XX
XX PS Claim 1; Page 42-43; 55pp; English.
XX
XX CC This protein comprises human neuronal attachment factor-1 (NAF-1), a
XX novel protein that promotes cell-cell interaction and cell adhesion. Its
XX amino acid sequence was deduced from a DNA molecule (see AAT78360)
XX isolated from a cDNA library derived from human epithelial sarcoma. NAF-1
XX shows sequence homology to the rat F-spondin family. NAF-1 polypeptides,
XX especially the mature protein, can be expressed in host cells. It can be
XX used e.g. to treat spinal cord injuries or damage to peripheral nerves by
XX promoting neural cell adhesion and neurite extension, to inhibit tumour
XX cell metastases, inhibit endothelial cell proliferation, adhesion and
XX motility, to decrease tumour neovascularisation, to be angiostatic for
XX tumours, to promote wound healing, and to modulate haemostasis. It can
XX also be used to screen for agonists and for antagonists useful e.g. in
XX the prevention of malaria
XX
XX SQ Sequence 331 AA;
XX
XX Query Match 100.0%; Score 85; DB 2; Length 331;
XX Best Local Similarity 100.0%; Pred. No. 1e-05;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 HSSDYSWVRKNQYVS 15
XX
XX Db 77 HSSDYSWVRKNQYVS 91
XX
XX RESULT 5
XX AAW70589
XX ID AAW70589 standard; protein; 331 AA.
XX
XX AC AAW70589;
XX
XX DT 01-MAR-1999 (first entry)
XX
XX DE Human mindin polypeptide.
XX
XX KW Mindin; human; integrin ligand; angiogenic disease; cancer; metastasis;
XX chronic inflammatory disorder; rheumatoid arthritis; atherosclerosis;
XX macular degeneration, diabetic retinopathy; restenosis;
XX KW Alzheimer's disease; neural disorder; tissue remodelling; therapy;
XX diagnosis.
XX
XX OS Homo sapiens.
XX
XX PN WO9850073-A1.
XX
XX AC AAW70589;

```

```

XX
XX DT 21-JAN-1999 (first entry)
XX
XX DE Adhesion-modulating protein zsig25.
XX
XX KW zsig25; adhesion-modulating protein; prostate cell; prostatic carcinoma;
XX B-cell cancer; infertility; Wolf-Hirschhorn syndrome;
XX KW chromosome 4 (p16.3).
XX
XX OS Homo sapiens.
XX
XX PN WO9845442-A2.
XX
XX PD 15-OCT-1998.
XX
XX PF 10-APR-1998; 98WO-US007117.
XX
XX PR 10-APR-1997; 97US-0043421P.
XX PR 11-JUN-1997; 97US-0049288P.
XX
XX PA (ZYMO) ZYMOGENETICS INC.
XX
XX PI Sheppard PO;
XX
XX DR WPI: 1998-557522/47.
XX DR N-PSDB; AAV63241.
XX
XX PT New zsig25 protein - and antibodies, involved in modulation of adhesion,
XX used for diagnosis and treatment of prostatic and B-cell tumours,
XX stimulation of haematopoietic cells, treatment of immune deficiency etc.
XX
XX PS Claim 7; Page 111; 161pp; English.
XX
XX CC The present sequence represents a protein designated zsig25. The zsig25
XX protein is an adhesion-modulating protein expressed at very high level in
XX prostate cells. The protein is useful as a diagnostic marker for
XX prostatic carcinoma and B-cell cancers, possibly also for infertility,
XX and as a reagent for separating cancerous and non-cancerous cells. The
XX products may also be used to diagnose or treat Wolf-Hirschhorn syndrome,
XX associated with a deletion in the region of chromosome 4 (p16.3) where
XX the zsig25 gene is located
XX
XX SQ Sequence 331 AA;
XX
XX Query Match 100.0%; Score 85; DB 2; Length 331;
XX Best Local Similarity 100.0%; Pred. No. 1e-05;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 HSSDYSWVRKNQYVS 15
XX
XX Db 77 HSSDYSWVRKNQYVS 91
XX
XX RESULT 6
XX AAW83328
XX ID AAW83328 standard; protein; 331 AA.
XX
XX AC AAW83328;
XX
XX DT 01-MAR-1999 (first entry)
XX
XX DE Human mindin polypeptide.
XX
XX KW Mindin; human; integrin ligand; angiogenic disease; cancer; metastasis;
XX chronic inflammatory disorder; rheumatoid arthritis; atherosclerosis;
XX macular degeneration, diabetic retinopathy; restenosis;
XX KW Alzheimer's disease; neural disorder; tissue remodelling; therapy;
XX diagnosis.
XX
XX OS Homo sapiens.
XX
XX PN WO9850073-A1.
XX
XX AC AAW83328;

```

PD 12-NOV-1998.  
XX  
PF 07-MAY-1998; 98WO-US009476.  
XX  
XX 09-MAY-1997; 97US-0046106P.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
XX  
XX Jonak ZL, Trulli SH, Tsui F, Lane PA;  
XX  
XX WPI; 1999-034688/03.  
DR N-PSDB; AAV72537.  
XX  
XX A new polypeptide is the integrin ligand, human mindin - useful in  
PT therapy and diagnostic assays for diseases such as those associated with  
PT angiogenesis.  
XX  
XX Claim 1; Page 29; 39pp; English.  
XX  
XX This is the amino acid sequence of human mindin, a novel integrin ligand.  
CC It has homology to F spondin, and may have a multifunctional activity in  
CC normal and disease states. The invention provides human mindin  
CC polypeptides and polynucleotides (see also AAV72537-38) and methods for  
CC producing such polypeptides by recombinant techniques. It also relates to  
CC methods for using such polypeptides and polynucleotides in the treatment  
CC of angiogenic diseases (cancer, cancer metastasis, chronic inflammation,  
CC disorders, rheumatoid arthritis, atherosclerosis, macular degeneration,  
CC diabetic retinopathy), restenosis, Alzheimer's disease, neural disorders  
CC and tissue remodelling. The invention also relates to methods for  
CC identifying agonists and antagonists/inhibitors and for treating  
CC conditions associated with human mindin imbalance with the identified  
CC compounds. Diagnostic assays for detecting diseases associated with  
CC inappropriate human mindin activity or levels are also claimed  
XX  
XX Sequence 331 AA;  
SQ

Query Match 100.0%; Score 85; DB 2; Length 331;  
Best Local Similarity 100.0%; Pred. NO. 1e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSSDYSMWKKNQYVS 15  
Db 77 HSSDYSMWKKNQYVS 91  
|||||

RESULT 7  
AAV41721  
ID AAV41721 standard; protein; 331 AA.  
XX  
XX AAV41721;  
XX  
XX 07-DEC-1999 (first entry)  
DT  
XX  
DE Human PRO866 protein sequence.  
XX  
XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;  
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
KW secreted protein; transmembrane protein.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO9946281-A2.  
XX  
XX 16-SEP-1999.  
PD  
XX  
XX 08-MAR-1999; 99WO-US005028.  
PF  
XX  
XX 10-MAR-1998; 98US-0077450P.  
PR  
XX 11-MAR-1998; 98US-0077632P.  
PR  
XX 11-MAR-1998; 98US-0077641P.  
PR  
XX 11-MAR-1998; 98US-0077649P.  
PR  
XX 12-MAR-1998; 98US-0077791P.  
PR  
XX 13-MAR-1998; 98US-0078004P.

PR 17-MAR-1998; 98US-00040220.  
PR 20-MAR-1998; 98US-0078886P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 20-MAR-1998; 98US-0078936P.  
PR 20-MAR-1998; 98US-0078939P.  
PR 25-MAR-1998; 98US-0079294P.  
PR 26-MAR-1998; 98US-0079656P.  
PR 26-MAR-1998; 98US-0079663P.  
PR 27-MAR-1998; 98US-0079664P.  
PR 27-MAR-1998; 98US-0079689P.  
PR 27-MAR-1998; 98US-0079728P.  
PR 27-MAR-1998; 98US-0079786P.  
PR 30-MAR-1998; 98US-0079920P.  
PR 30-MAR-1998; 98US-0079923P.  
PR 31-MAR-1998; 98US-0080105P.  
PR 31-MAR-1998; 98US-0080107P.  
PR 31-MAR-1998; 98US-0080165P.  
PR 31-MAR-1998; 98US-0080194P.  
PR 01-APR-1998; 98US-0080327P.  
PR 01-APR-1998; 98US-0080328P.  
PR 01-APR-1998; 98US-0080333P.  
PR 01-APR-1998; 98US-0080334P.  
PR 08-APR-1998; 98US-0081049P.  
PR 08-APR-1998; 98US-0081070P.  
PR 08-APR-1998; 98US-0081071P.  
PR 09-APR-1998; 98US-0081195P.  
PR 09-APR-1998; 98US-0081203P.  
PR 09-APR-1998; 98US-0081229P.  
PR 15-APR-1998; 98US-0081817P.  
PR 15-APR-1998; 98US-0081838P.  
PR 15-APR-1998; 98US-0081952P.  
PR 15-APR-1998; 98US-0081955P.  
PR 21-APR-1998; 98US-0082568P.  
PR 21-APR-1998; 98US-0082569P.  
PR 22-APR-1998; 98US-0082700P.  
PR 22-APR-1998; 98US-0082704P.  
PR 22-APR-1998; 98US-0082804P.  
PR 23-APR-1998; 98US-0082767P.  
PR 23-APR-1998; 98US-0082796P.  
PR 28-APR-1998; 98US-0083336P.  
PR 28-APR-1998; 98US-0083322P.  
PR 29-APR-1998; 98US-0083392P.  
PR 29-APR-1998; 98US-0083495P.  
PR 29-APR-1998; 98US-0083496P.  
PR 29-APR-1998; 98US-0083499P.  
PR 29-APR-1998; 98US-0083500P.  
PR 29-APR-1998; 98US-0083545P.  
PR 29-APR-1998; 98US-0083554P.  
PR 29-APR-1998; 98US-0083558P.  
PR 30-APR-1998; 98US-0083559P.  
PR 30-APR-1998; 98US-0083742P.  
PR 05-MAY-1998; 98US-0084366P.  
PR 06-MAY-1998; 98US-0084414P.  
PR 06-MAY-1998; 98US-0084441P.  
PR 07-MAY-1998; 98US-0084598P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 07-MAY-1998; 98US-0084627P.  
PR 07-MAY-1998; 98US-0084637P.  
PR 07-MAY-1998; 98US-0084639P.  
PR 07-MAY-1998; 98US-0084640P.  
PR 07-MAY-1998; 98US-0084643P.  
PR 13-MAY-1998; 98US-0085323P.  
PR 13-MAY-1998; 98US-0085338P.  
PR 13-MAY-1998; 98US-0085339P.  
PR 15-MAY-1998; 98US-0085573P.  
PR 15-MAY-1998; 98US-0085579P.  
PR 15-MAY-1998; 98US-0085580P.  
PR 15-MAY-1998; 98US-0085582P.  
PR 15-MAY-1998; 98US-0085689P.  
PR 15-MAY-1998; 98US-0085697P.  
PR 15-MAY-1998; 98US-0085700P.  
PR 15-MAY-1998; 98US-0085704P.  
PR 18-MAY-1998; 98US-0086023P.

PR 22-MAY-1998; 98US-0086392P.  
 PR 22-MAY-1998; 98US-0086414P.  
 PR 22-MAY-1998; 98US-0086430P.  
 PR 28-MAY-1998; 98US-0086486P.  
 PR 28-MAY-1998; 98US-0087098P.  
 PR 28-MAY-1998; 98US-0087106P.  
 PR 28-MAY-1998; 98US-0087208P.  
 PR 30-JUL-1998; 98US-0094651P.  
 PR 11-SEP-1998; 98US-0100038P.  
 XX (GETH ) GENENTECH INC.  
 PA Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;  
 PI WPI; 1999-551358/46.  
 XX N-PSDB; AAZ34089.  
 XX New secreted and transmembrane polypeptides and their polynucleotides,  
 PT useful for treating blood coagulation disorders, cancers and cellular  
 PT adhesion disorders.  
 XX Claim 12; Fig 87; 530pp; English.  
 XX The present invention describes secreted and transmembrane polypeptides  
 CC and their polynucleotides. The nucleotide sequences are useful as sources  
 CC of probes, primers, for chromosome mapping, and for generation of  
 CC antisense sequences. They can also be used to create transgenic animals.  
 CC The proteins can be used to treat a variety of diseases and disorders,  
 CC depending on their function. Diseases that may be treated include blood  
 CC coagulation disorders, cancers and cellular adhesion disorders. They may  
 CC also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to  
 CC AAY41774 represent polynucleotide and polypeptide sequence given in the  
 CC exemplification of the present invention  
 XX SQ Sequence 331 AA;  
 Query Match 100.0%; Score 85; DB 2; Length 331;  
 Best Local Similarity 100.0%; Pred. No. 1e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HSSDYSWMRKQYVS 15  
 |||||  
 DB 77 HSSDYSWMRKQYVS 91  
 RESULT 8  
 AAW92460  
 ID AAW92460 standard; protein; 331 AA.  
 XX AAW92460;  
 XX 21-APR-1999 (first entry)  
 XX Human NAP-1 protein.  
 XX NAP-1; neuronal attachment factor-1; F-spondin analogue; treatment;  
 KW spinal cord injury; peripheral nerves damage; neural cell adhesion;  
 KW neurite extension; tumour cell metastasis; inhibitor; mobility; disease;  
 KW endothelial cell proliferation; tumour neovascularisation; haemostasis;  
 KW angiostatic agent; wound healing; diagnostic; neurotrophic; anticancer;  
 KW antimetastatic; anti-angiogenic; antimalarial; human.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH Peptide 1..23  
 FT /label= signal\_peptide  
 FT Protein 24..331  
 XX US5871969-A.  
 XX 16-FEB-1999.  
 XX

PF 12-FEB-1997; 97US-00799173.  
 XX 12-FEB-1996; 96US-0011519P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX Dillon PJ, Hastings G;  
 XX WPI; 1999-166644/14.  
 DR N-PSDB; AAX02019.  
 XX Nucleic acid encoding human neuronal attachment factor-1 - used to e.g.  
 PT treat spinal cord injuries, and inhibit tumor cell metastasis and  
 PT neovascularization.  
 XX Claim 1a; Fig 1; 29pp; English.  
 XX This sequence represents a novel human neuronal attachment factor-1, NAP-  
 CC 1. NAP-1 is an analogue of rat F-spondin and is used to treat spinal cord  
 CC injuries and damage to peripheral nerves (by promoting neural cell  
 CC adhesion and neurite extension), to inhibit tumor cell metastasis  
 CC (particularly in small cell and breast carcinoma) and endothelial cell  
 CC proliferation, adhesion and mobility, to reduce tumor neovascularization,  
 CC as angiostatic agents for tumor cells, to promote wound healing and to  
 CC modulate hemostasis. NAP-1 may also be used to identify treatments and  
 CC diagnoses for human disease. Fragments of the nucleic acid that do not  
 CC encode NAP-1 peptides are useful as probes to isolate the NAP-1 gene, its  
 CC allelic variants, full-length cDNA or related sequences, in chromosomal  
 CC location by in situ hybridization or in Northern blotting, and as  
 CC diagnostic probes or primers. The protein has neurotrophic, anticancer,  
 CC antimetastatic, anti-angiogenic, antimalarial and modulates adhesion,  
 CC proliferation and mobility of cells  
 XX SQ Sequence 331 AA;  
 Query Match 100.0%; Score 85; DB 2; Length 331;  
 Best Local Similarity 100.0%; Pred. No. 1e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HSSDYSWMRKQYVS 15  
 |||||  
 DB 77 HSSDYSWMRKQYVS 91  
 RESULT 9  
 AAB33465  
 ID AAB33465 standard; protein; 331 AA.  
 XX AAB33465;  
 XX 29-JAN-2001 (first entry)  
 XX Human PRO866 protein UNQ435 SEQ ID NO:258.  
 XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;  
 KW dermatological; antiarthritic; antirheumatic; immunosuppressive;  
 KW haemostatic; antithyroid; antidiabetic; neurotrophic; neuroprotective;  
 KW antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;  
 KW osteoarthritic; systemic lupus erythematosus; rheumatoid arthritis;  
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
 KW autoimmune thrombocytopaenia; immune-mediated renal disease;  
 KW demyelinating disease; hepatobiliary disease; Whipple's disease;  
 KW inflammatory bowel disease; gluten-sensitive enteropathy;  
 KW autoimmune disease; immune-mediated skin disease; allergic disease;  
 KW immunological disease; transplantation associated disease;  
 KW graft rejection; graft-versus-host-disease.  
 XX Homo sapiens.  
 OS  
 XX WO2000053758-A2.  
 XX

PD 14-SEP-2000.  
XX 02-MAR-2000; 2000WO-US005941.  
XX 08-MAR-1999; 99WO-US005028.  
XX 10-MAR-1999; 99US-0123618P.  
XX 12-MAR-1999; 99US-0123957P.  
XX 13-MAR-1999; 99US-0125775P.  
XX 12-APR-1999; 99WO-US028849P.  
XX 20-APR-1999; 99WO-US008615.  
XX 28-APR-1999; 99US-0131445P.  
XX 04-MAY-1999; 99US-0132371P.  
XX 14-MAY-1999; 99US-0134287P.  
XX 02-JUN-1999; 99WO-US012252.  
XX 23-JUN-1999; 99US-0141037P.  
XX 26-JUL-1999; 99US-0144758P.  
XX 26-JUL-1999; 99US-0145638P.  
XX 28-JUL-1999; 99US-0146222P.  
XX 01-SEP-1999; 99WO-US020111.  
XX 08-SEP-1999; 99WO-US020594.  
XX 13-SEP-1999; 99WO-US020944.  
XX 15-SEP-1999; 99WO-US021090.  
XX 15-SEP-1999; 99WO-US021547.  
XX 03-OCT-1999; 99WO-US023089.  
XX 29-OCT-1999; 99US-0162506P.  
XX 29-NOV-1999; 99WO-US028214.  
XX 30-NOV-1999; 99WO-US028313.  
XX 01-NOV-1999; 99WO-US028409.  
XX 01-DEC-1999; 99WO-US028301.  
XX 01-DEC-1999; 99WO-US028634.  
XX 02-DEC-1999; 99WO-US028551.  
XX 02-DEC-1999; 99WO-US028564.  
XX 02-DEC-1999; 99WO-US028565.  
XX 16-DEC-1999; 99WO-US030095.  
XX 20-DEC-1999; 99WO-US030399.  
XX 30-DEC-1999; 99WO-US031274.  
XX 05-JAN-2000; 2000WO-US000219.  
XX 06-JAN-2000; 2000WO-US000277.  
XX 06-JAN-2000; 2000WO-US000376.  
XX 11-FEB-2000; 2000WO-US003565.  
XX 18-FEB-2000; 2000WO-US004341.  
XX 18-FEB-2000; 2000WO-US004342.  
XX 22-FEB-2000; 2000WO-US004414.  
XX (GETH ) GENENTECH INC.  
XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
XX Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;  
XX Stewart TA, Tamas D, Watanabe CK, Wood WI, Yan M;  
XX WPI; 2000-572271/53.  
XX N-PSDB; AAC58630.  
XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
XX immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
XX arthritis, osteoarthritis, thyroiditis and diabetes mellitus.  
XX Claim 33; Fig 104; 309pp; English.  
XX The present invention describes sixty four human PRO proteins which can  
XX be used in the treatment of immune related diseases. The human PRO  
XX proteins, anti-PRO antibodies, agonists and antagonists are useful for  
XX treating and diagnosing immune related disorders. The disorders are  
XX selected from systemic lupus erythematosus, rheumatoid arthritis,  
XX osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
XX systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
XX syndrome, autoimmune vasculitis, sarcoidosis, autoimmune haemolytic  
XX anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
XX immune-mediated renal disease, demyelinating diseases of the central and  
XX peripheral nervous systems, hepatobiliary diseases, inflammatory bowel  
XX disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune  
XX or immune-mediated skin diseases, allergic diseases, immunological  
XX diseases of the lung, and transplantation associated diseases including

CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578  
CC represent PCR primers and hybridisation probes used in the isolation of  
CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477  
CC represent human PRO polynucleotide and protein sequences given in the  
CC exemplification of the present invention  
XX Sequence 331 AA;  
SQ  
Query Match 100.0%; Score 85; DB 3; Length 331;  
Best Local Similarity 100.0%; Pred. No. 1e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 HSSDYSMMRKQYVS 15  
Db 77 HSSDYSMMRKQYVS 91  
|||||  
RESULT 10  
AAAY79561  
ID AAY79561 standard; protein; 331 AA.  
XX AC AAY79561;  
XX DT 15-AUG-2000 (first entry)  
XX DE Cancer specific protein Pro108 useful as prostate cancer marker.  
XX KW Cancer specific gene; CSG; prostate cancer; diagnosis; monitoring;  
XX KW staging; imaging; metastasis; therapy; human; Pro108.  
XX OS Homo sapiens.  
XX PN WO200023108-A1.  
XX PD 27-APR-2000.  
XX PF 18-OCT-1999; 99WO-US023764.  
XX PR 19-OCT-1998; 98US-0104741P.  
XX PA (DIAD-) DIADEXUS LLC.  
XX PI Ali SM, Sun Y, Salceda S, Recipon H, Cafferkey R;  
XX WPI; 2000-339528/29.  
XX DR N-PSDB; AAZ95034.  
XX PT Diagnosing, detecting, staging, monitoring, imaging and treating cancers,  
XX especially useful for detecting prostate cancer comprises measuring  
XX changes in levels of cancer specific genes in cells, tissues and body  
XX fluids.  
XX PS Claim 6; Page 29-30; 35pp; English.  
XX The present sequence is that of the protein encoded by human cancer  
XX specific gene (CSG) pro108 (see AAZ95034). The CSG was identified using a  
XX suppression subtractive hybridization method. It is a diagnostic marker  
XX for prostate cancer. In 11 different healthy tissues examined, pro108  
XX mRNA expression was highest in the ovary and uterus. Expression in  
XX healthy prostate was low. However, overexpression of CSG pro108 was  
XX observed in 13 of 13 prostate cancer tissues examined. CSGs comprising  
XX pro108, the encoded polypeptide, or an antibody that specifically binds  
XX CSG, are used in claimed methods for the diagnosis, detection, staging,  
XX monitoring, imaging and treatment of prostate cancer. The new methods  
XX provide earlier diagnosis for the presence and metastasis of prostate  
XX cancer, and can be used to determine if a cancer has metastasized, or to  
XX monitor the progress or stage of the disease when it has not metastasized  
XX Sequence 331 AA;  
SQ  
Query Match 100.0%; Score 85; DB 3; Length 331;  
Best Local Similarity 100.0%; Pred. No. 1e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSSDYSWVRKNQYVS 15  
 Db 77 HSSDYSWVRKNQYVS 91

RESULT 11  
 AAB44277 AAB44277 standard; protein; 331 AA.

XX  
 AC AAB44277;  
 XX  
 DT 08-FEB-2001 (first entry)  
 XX  
 DE Human PRO866 (UNQ435) protein sequence SEQ ID NO:236.  
 XX  
 KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;  
 KW expressed sequence tag; detection; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200053756-A2.  
 XX  
 PD 14-SEP-2000.  
 XX  
 PF 18-FEB-2000; 2000WO-US004341.  
 XX  
 PR 08-MAR-1999; 99WO-US005028.  
 PR 12-MAR-1999; 99US-0123957P.  
 PR 29-MAR-1999; 99US-0126773P.  
 PR 21-APR-1999; 99US-0130232P.  
 PR 28-APR-1999; 99US-0131445P.  
 PR 14-MAY-1999; 99US-0134287P.  
 PR 23-JUN-1999; 99US-0141037P.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 29-OCT-1999; 99US-0162506P.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 02-DEC-1999; 99WO-US028551.  
 PR 16-DEC-1999; 99WO-US028565.  
 PR 30-DEC-1999; 99WO-US030095.  
 PR 30-DEC-1999; 99WO-US031243.  
 PR 05-JAN-2000; 99WO-US031274.  
 PR 06-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000277.  
 PR 06-JAN-2000; 2000WO-US000376.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;  
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
 PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;  
 PI Stewart TA, Tumas D, Williams PM, Wood WI;  
 XX  
 DR WPI; 2000-611443/58.  
 DR N-PSDB; AAC78507.  
 XX  
 PT Novel PRO polypeptides and polynucleotides used in detection methods, to  
 PT target bioactive molecules to specific cells, and to modulate cellular  
 PT activities.  
 XX  
 PS Claim 12; Fig 87; 636pp; English.  
 XX  
 CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence  
 CC tag) sequences which encode secreted or transmembrane PRO polypeptides.  
 CC The PRO polynucleotides and polypeptides have cytostatic activity. The  
 CC polynucleotides and polypeptides can be used for detecting the presence  
 CC of PRO polypeptides in samples, for linking bioactive molecules to cells  
 CC and for modulating biological activities of cells, using the polypeptides  
 CC for specific targeting. The polypeptide targeting can be used to kill the  
 CC target cells, e.g. for the treatment of cancers. The polypeptide pairs  
 CC provide specific targeting of bioactive molecules to cells. AAC78600 to  
 CC AAC78987 represent PCR primers and probes used in the isolation of the

CC PRO polynucleotide sequences  
 XX Sequence 331 AA;  
 SQ

Query Match 100.0%; Score 85; DB 3; Length 331;  
 Best Local Similarity 100.0%; Pred. No. 1e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSSDYSWVRKNQYVS 15  
 Db 77 HSSDYSWVRKNQYVS 91

RESULT 12  
 AAY95349  
 ID AAY95349 standard; protein; 331 AA.  
 XX  
 AC AAY95349;  
 XX  
 DT 25-SEP-2000 (first entry)  
 XX  
 DE Human PRO866 antitumour protein.  
 XX  
 KW PRO866; human; antitumour; tumour; therapy; cytostatic; breast cancer;  
 KW ovarian cancer; renal cancer; colorectal cancer; uterine cancer;  
 KW prostate cancer; lung cancer; bladder cancer;  
 KW central nervous system cancer; melanoma; leukaemia; neoplasm.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..26 /label= Signal\_peptide  
 FT Modified-site 26..32 /note= "N-myristoylation"  
 FT Protein 27..331 /label= PRO866  
 FT Modified-site 74..80 /note= "N-myristoylation"  
 FT Region 131..135 /note= "glycosaminoglycan attachment site"  
 FT Modified-site 132..138 /note= "N-myristoylation"  
 FT Modified-site 134..140 /note= "N-myristoylation"  
 FT Modified-site 144..148 /note= "protein kinase phosphorylation site"  
 FT Modified-site 190..196 /note= "N-myristoylation"  
 FT Modified-site 287..293 /note= "N-myristoylation"  
 FT Modified-site 290..296 /note= "N-myristoylation"  
 XX  
 PN WO200037638-A2.  
 XX  
 PD 29-JUN-2000.  
 XX  
 PF 02-DEC-1999; 99WO-US028565.  
 XX  
 PR 22-DEC-1998; 98US-0113296P.  
 PR 08-MAR-1999; 99WO-US0005028.  
 PR 21-APR-1999; 99US-0130232P.  
 PR 28-APR-1999; 99US-0131445P.  
 PR 14-MAY-1999; 99US-0134287P.  
 PR 20-JUL-1999; 99US-0144758P.  
 PR 28-JUL-1999; 99US-0145698P.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Marsters SA;

PI Napier MA, Pitti RM, Wood WI;  
 XX WPI; 2000-442668/38.  
 DR N-PSDB; AAA49728.  
 XX  
 PT Novel composition to inhibit neoplastic cell growth or for treating tumor  
 PT in mammal comprises polypeptides PRO179, PRO207, PRO320, PRO219, PRO221,  
 PT PRO224, PRO328, PRO301, PRO326, PRO362, PRO356, PRO509 or PRO866.  
 XX  
 PS Claim 19; Fig 26; 172pp; English.  
 XX  
 CC The present sequence is that of human antitumour protein PRO866, as  
 CC deduced from a foetal kidney cDNA clone (see AAA49728). PRO866 shows  
 CC homology to members of the mindin/spondin family of proteins. A claimed  
 CC method for inhibiting the growth of a tumour cell comprises exposing the  
 CC tumor cell to PRO179, PRO207, PRO320, PRO219, PRO221, PRO224, PRO328,  
 CC PRO301, PRO326, PRO362, PRO356, PRO509 or PRO866 (see AAY95337-49), their  
 CC agonists or chimeric polypeptides incorporating them. The tumour is  
 CC especially a cancer selected from breast, ovarian, renal, colorectal,  
 CC uterine, prostate, lung, bladder and central nervous system cancer,  
 CC melanoma and leukaemia. Methods for the recombinant expression of the  
 CC antitumour proteins are also provided  
 XX  
 SQ Sequence 331 AA;  
 Query Match 100.0%; Score 85; DB 3; Length 331;  
 Best Local Similarity 100.0%; Pred. No. 1e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HSSDYSWVRKNQYVS 15  
 Db |||||  
 77 HSSDYSWVRKNQYVS 91  
 RESULT 13  
 AAM93266  
 ID AAM93266 standard; protein; 331 AA.  
 AC AAM93266;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Human polypeptide, SEQ ID NO: 2727.  
 DE  
 KW Human; full length cDNA; cDNA synthesis; oligo-capping.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1130094-A2.  
 XX  
 PD 05-SEP-2001.  
 XX  
 PF 07-JUL-2000; 2000EP-00114089.  
 XX  
 PR 08-JUL-1999; 99JP-00194486.  
 PR 11-JAN-2000; 2000JP-00118774.  
 PR 02-MAY-2000; 2000JP-00183765.  
 XX  
 PA (HELI-) HELIX RES INST.  
 XX  
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
 XX  
 DR WPI; 2001-524255/58.  
 DR N-PSDB; AAK94182.  
 XX  
 CC 830 Primers useful for synthesizing full length cDNA clones and their use  
 CC in genetic manipulation.  
 CC  
 PS Claim 8; SEQ ID NO 2727; 1380pp + Sequence Listing; English.  
 XX  
 CC The invention relates to primers for synthesizing full length cDNA  
 CC clones. 830 cDNA molecules encoding a human protein have been isolated  
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have  
 CC been determined. Primers for synthesizing the full length cDNA are useful  
 CC for clarifying the function of the protein encoded by the cDNA. The full  
 CC length clones were obtained by construction of full length enriched cDNA  
 CC libraries that were synthesised by the oligo-capping method. The primers  
 CC enable the production of the full length cDNA easily without any special  
 CC methods. The present sequence is a polypeptide encoded by a full length  
 CC human cDNA of the invention. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in CD-ROM  
 CC format directly from EPO  
 XX  
 SQ Sequence 331 AA;  
 Query Match 100.0%; Score 85; DB 3; Length 331;  
 Best Local Similarity 100.0%; Pred. No. 1e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HSSDYSWVRKNQYVS 15  
 Db |||||  
 77 HSSDYSWVRKNQYVS 91  
 RESULT 14  
 AAM93324  
 ID AAM93324 standard; protein; 331 AA.  
 AC AAM93324;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Human polypeptide, SEQ ID NO: 2847.  
 DE  
 KW Human; full length cDNA; cDNA synthesis; oligo-capping.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1130094-A2.  
 XX  
 PD 05-SEP-2001.  
 XX  
 PF 07-JUL-2000; 2000EP-00114089.  
 XX  
 PR 08-JUL-1999; 99JP-00194486.  
 PR 11-JAN-2000; 2000JP-00118774.  
 PR 02-MAY-2000; 2000JP-00183765.  
 XX  
 PA (HELI-) HELIX RES INST.  
 XX  
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
 XX  
 DR WPI; 2001-524255/58.  
 DR N-PSDB; AAK94244.  
 XX  
 CC 830 Primers useful for synthesizing full length cDNA clones and their use  
 CC in genetic manipulation.  
 CC  
 PS Claim 8; SEQ ID NO 2847; 1380pp + Sequence Listing; English.  
 XX  
 CC The invention relates to primers for synthesizing full length cDNA  
 CC clones. 830 cDNA molecules encoding a human protein have been isolated  
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have  
 CC been determined. Primers for synthesizing the full length cDNA are useful  
 CC for clarifying the function of the protein encoded by the cDNA. The full  
 CC length clones were obtained by construction of full length enriched cDNA  
 CC libraries that were synthesised by the oligo-capping method. The primers  
 CC enable the production of the full length cDNA easily without any special  
 CC methods. The present sequence is a polypeptide encoded by a full length  
 CC human cDNA of the invention. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in CD-ROM  
 CC format directly from EPO  
 XX  
 SQ Sequence 331 AA;

CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have  
 CC been determined. Primers for synthesising the full length cDNA are useful  
 CC for clarifying the function of the protein encoded by the cDNA. The full  
 CC length clones were obtained by construction of full length enriched cDNA  
 CC libraries that were synthesised by the oligo-capping method. The primers  
 CC enable the production of the full length cDNA easily without any special  
 CC methods. The present sequence is a polypeptide encoded by a full length  
 CC human cDNA of the invention. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in CD-ROM  
 CC format directly from EPO  
 XX  
 SQ Sequence 331 AA;  
 Query Match 100.0%; Score 85; DB 4; Length 331;  
 Best Local Similarity 100.0%; Pred. No. 1e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HSSDYSWVRKNQYVS 15  
 Db |||||  
 77 HSSDYSWVRKNQYVS 91  
 RESULT 14  
 AAM93324  
 ID AAM93324 standard; protein; 331 AA.  
 AC AAM93324;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Human polypeptide, SEQ ID NO: 2847.  
 DE  
 KW Human; full length cDNA; cDNA synthesis; oligo-capping.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1130094-A2.  
 XX  
 PD 05-SEP-2001.  
 XX  
 PF 07-JUL-2000; 2000EP-00114089.  
 XX  
 PR 08-JUL-1999; 99JP-00194486.  
 PR 11-JAN-2000; 2000JP-00118774.  
 PR 02-MAY-2000; 2000JP-00183765.  
 XX  
 PA (HELI-) HELIX RES INST.  
 XX  
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
 XX  
 DR WPI; 2001-524255/58.  
 DR N-PSDB; AAK94244.  
 XX  
 CC 830 Primers useful for synthesizing full length cDNA clones and their use  
 CC in genetic manipulation.  
 CC  
 PS Claim 8; SEQ ID NO 2847; 1380pp + Sequence Listing; English.  
 XX  
 CC The invention relates to primers for synthesising full length cDNA  
 CC clones. 830 cDNA molecules encoding a human protein have been isolated  
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have  
 CC been determined. Primers for synthesising the full length cDNA are useful  
 CC for clarifying the function of the protein encoded by the cDNA. The full  
 CC length clones were obtained by construction of full length enriched cDNA  
 CC libraries that were synthesised by the oligo-capping method. The primers  
 CC enable the production of the full length cDNA easily without any special  
 CC methods. The present sequence is a polypeptide encoded by a full length  
 CC human cDNA of the invention. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in CD-ROM  
 CC format directly from EPO  
 XX  
 SQ Sequence 331 AA;

Query Match 100.0%; Score 85; DB 4; Length 331;  
 Best Local Similarity 100.0%; Pred. No. 1e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSSDYSWRRKNQYVS 15  
 |||||  
 DB 77 HSSDYSWRRKNQYVS 91

RESULT 15  
 AAM38872  
 ID AAM38872 standard; protein; 331 AA.  
 XX AC AAM38872,  
 XX DT 22-OCT-2001 (first entry)  
 XX DE Human polypeptide SEQ ID NO 2017.  
 XX KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukaemia.  
 XX OS Homo sapiens.  
 XX PN WO200153312-A1.  
 XX PD 26-JUL-2001.  
 XX PF 26-DEC-2000; 2000WO-US034263.  
 XX PR 23-DEC-1999; 99US-00471275.  
 PR 21-JAN-2000; 2000US-00488725.  
 PR 25-APR-2000; 2000US-00552317.  
 PR 20-JUN-2000; 2000US-00598042.  
 PR 19-JUL-2000; 2000US-00620312.  
 PR 03-AUG-2000; 2000US-00653450.  
 PR 14-SEP-2000; 2000US-00662191.  
 PR 19-OCT-2000; 2000US-00693036.  
 PR 29-NOV-2000; 2000US-00727344.  
 XX PA (HYSE-) HYSEQ INC.  
 XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
 PI Zhou P, Goodrich R, Drmanac RT;  
 XX WPI; 2001-442253/47.  
 DR N-PSDB; AAI58028.  
 XX PT Novel nucleic acids and polypeptides, useful for treating disorders such  
 PT as central nervous system injuries.  
 XX PS Example 3; SEQ ID NO 2017; 10078pp; English.  
 XX CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the  
 CC encoded polypeptides (AAM38642-AAM42213) with nootropic,  
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localised neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: Immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemias and  
 CC C.N.S disorders. Note: The sequence data for this patent did not form

CC part of the printed specification  
 XX SQ Sequence 331 AA;  
 Query Match 100.0%; Score 85; DB 4; Length 331;  
 Best Local Similarity 100.0%; Pred. No. 1e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSSDYSWRRKNQYVS 15  
 |||||  
 DB 77 HSSDYSWRRKNQYVS 91

Search completed: June 3, 2005, 08:21:44  
 Job time : 16.825 secs

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OM protein - protein search, using sw model

Run on: June 3, 2005, 08:28:22 ; Search time 12.15 Seconds  
(without alignments)  
426.765 Million cell updates/sec

Title: US-10-616-279-10

Perfect score: 85

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Searched: 1465611 seqs, 345679903 residues

Total number of hits satisfying chosen parameters: 1465611

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
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- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	15	9 US-09-732-357A-10	Sequence 10, Appl
2	85	100.0	15	15 US-10-616-279-10	Sequence 10, Appl
3	85	100.0	15	16 US-10-624-884-10	Sequence 10, Appl
4	85	100.0	15	17 US-10-895-183-10	Sequence 10, Appl
5	85	100.0	290	15 US-10-629-952-4	Sequence 4, Appli
6	85	100.0	330	9 US-09-903-383-2	Sequence 2, Appli
7	85	100.0	331	9 US-09-732-357A-2	Sequence 2, Appli
8	85	100.0	331	9 US-09-978-295A-236	Sequence 236, App
9	85	100.0	331	9 US-09-938-418-8	Sequence 8, Appli
10	85	100.0	331	9 US-09-978-697-236	Sequence 236, App
11	85	100.0	331	9 US-09-978-192A-236	Sequence 236, App
12	85	100.0	331	9 US-09-999-832A-236	Sequence 236, App
13	85	100.0	331	10 US-09-978-189-236	Sequence 236, App

14	85	100.0	331	10 US-09-978-608A-236	Sequence 236, App
15	85	100.0	331	10 US-09-978-585A-236	Sequence 236, App
16	85	100.0	331	10 US-09-978-191A-236	Sequence 236, App
17	85	100.0	331	10 US-09-978-403A-236	Sequence 236, App
18	85	100.0	331	10 US-09-978-564A-236	Sequence 236, App
19	85	100.0	331	10 US-09-999-833A-236	Sequence 236, App
20	85	100.0	331	10 US-09-981-915A-236	Sequence 236, App
21	85	100.0	331	10 US-09-978-824-236	Sequence 236, App
22	85	100.0	331	10 US-09-918-585A-236	Sequence 236, App
23	85	100.0	331	10 US-09-999-834A-236	Sequence 236, App
24	85	100.0	331	10 US-09-978-423A-236	Sequence 236, App
25	85	100.0	331	10 US-09-978-193A-236	Sequence 236, App
26	85	100.0	331	10 US-09-999-830A-236	Sequence 236, App
27	85	100.0	331	10 US-09-978-757A-236	Sequence 236, App
28	85	100.0	331	10 US-09-978-187B-236	Sequence 236, App
29	85	100.0	331	10 US-09-978-643A-236	Sequence 236, App
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38	85	100.0	331	10 US-09-978-665A-236	Sequence 236, App
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40	85	100.0	331	10 US-09-970-944-12	Sequence 12, Appl
41	85	100.0	331	10 US-09-970-944-39	Sequence 39, Appl
42	85	100.0	331	10 US-09-970-944-40	Sequence 40, Appl
43	85	100.0	331	10 US-09-999-831A-236	Sequence 236, App
44	85	100.0	331	11 US-10-017-081A-236	Sequence 236, App
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#### ALIGNMENTS

RESULT 1  
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; Patent No. US20020004047A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkins, Richard  
; APPLICANT: Parkes, Deborah  
; APPLICANT: Parry, Gordon  
; APPLICANT: Schneider, Douglas  
; APPLICANT: Steinbrecher, Renate  
; TITLE OF INVENTION: DNA Encoding a No. US20020004047A1el RG-1 Polypeptide  
; FILE REFERENCE: 51791AUSM1  
; CURRENT APPLICATION NUMBER: US/09732,357A  
; CURRENT FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: 60/172,370  
; PRIOR FILING DATE: 1999-12-16  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-732-357A-10

Query Match 100.0%; Score 85; DB 9; Length 15;  
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US-10-616-279-10

; Sequence 10, Application US/10616279

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; Publication No. US20040023307A1
; GENERAL INFORMATION:
; APPLICANT: Harkins, Richard
; APPLICANT: Parkes, Deborah
; APPLICANT: Schneider, Douglas
; APPLICANT: Parry, Gordon
; APPLICANT: Steinbrecher, Renate
; TITLE OF INVENTION: DNA Encoding a No. US20040023307A1el RG-1 Polypeptide
; FILE REFERENCE: 51791AUSD1
; CURRENT APPLICATION NUMBER: US/10/616,279
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US 60/172,370
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: US 09/732,357
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-616-279-10

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Qy 1 HSSDYSWMRKNOYVS 15
Db 1 HSSDYSWMRKNOYVS 15

RESULT 3
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; Publication No. US20040152139A1
; GENERAL INFORMATION:
; APPLICANT: Harkins, Richard
; APPLICANT: Parkes, Deborah
; APPLICANT: Parry, Gordon
; APPLICANT: Schneider, Douglas
; APPLICANT: Steinbrecher, Renate
; TITLE OF INVENTION: DNA Encoding a Novel RG-1 Polypeptide
; FILE REFERENCE: 51791AUSC1
; CURRENT APPLICATION NUMBER: US/10/624,884
; CURRENT FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: US 60/172,370
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: US 09/732,357
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-624-884-10

Query Match      100.0%; Score 85; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSSDYSWMRKNOYVS 15
Db 1 HSSDYSWMRKNOYVS 15

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; Publication No. US20050019845A1
; GENERAL INFORMATION:
; APPLICANT: Harkins, Richard
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; APPLICANT: Parkes, Deborah
; APPLICANT: Parry, Gordon
; APPLICANT: Schneider, Douglas
; APPLICANT: Steinbrecher, Renate
; TITLE OF INVENTION: RG1 Antibodies and Uses Thereof
; FILE REFERENCE: 51791BUSM1
; CURRENT APPLICATION NUMBER: US/10/895,183
; CURRENT FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 60/489,032
; PRIOR FILING DATE: 2003-07-22
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-895-183-10

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Db 1 HSSDYSWMRKNOYVS 15

RESULT 5
US-10-629-952-4
; Sequence 4, Application US/10629952
; Publication No. US20040072227A1
; GENERAL INFORMATION:
; APPLICANT: Jonak, Zdenka L
; APPLICANT: Trulli, Stephen H
; APPLICANT: Tsui, Ping
; APPLICANT: Lane, Pamela A.
; TITLE OF INVENTION: INTEGRIN LIGAND, HUMAN MINDIN
; FILE REFERENCE: DDX-100US
; CURRENT APPLICATION NUMBER: US/10/629,952
; CURRENT FILING DATE: 2003-07-29
; NUMBER OF SEQ ID NOS: 4
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; SEQ ID NO 4
; LENGTH: 290
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-10-629-952-4

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Best Local Similarity 100.0%; Pred. No. 7.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSSDYSWMRKNOYVS 15
Db 77 HSSDYSWMRKNOYVS 91

RESULT 6
US-09-903-383-2
; Sequence 2, Application US/09903383
; Patent No. US20020137135A1
; GENERAL INFORMATION:
; APPLICANT: Sytkowski, Arthur J.
; APPLICANT: Yang, Meiheng
; TITLE OF INVENTION: NOVEL NFG-1 GENE THAT IS DIFFERENTIALLY EXPRESSED IN PROSTATE
; TITLE OF INVENTION: TUMORS
; FILE REFERENCE: 01948/053002
; CURRENT APPLICATION NUMBER: US/09/903,383
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/371,696
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/022,238
; PRIOR FILING DATE: 1998-02-11
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; PRIOR APPLICATION NUMBER: US 08/644,326  
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; ORGANISM: Homo sapiens  
US-09-903-383-2

Query Match 100.0%; Score 85; DB 9; Length 330;  
Best Local Similarity 100.0%; Pred. No. 8.6e-05;  
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QY 1 HSSDYSWVRKNQYVS 15  
Db 77 HSSDYSWVRKNQYVS 91  
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RESULT 7  
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; GENERAL INFORMATION:  
; APPLICANT: Harkins, Richard  
; APPLICANT: Parkes, Deborah  
; APPLICANT: Parry, Gordon  
; APPLICANT: Schneider, Douglas  
; APPLICANT: Steinbrecher, Renate  
; TITLE OF INVENTION: DNA Encoding a No. US20020004047A1el RG-1 Polypeptide  
; FILE REFERENCE: 51791AUSM1  
; CURRENT APPLICATION NUMBER: US/09/732,357A  
; CURRENT FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: 60/172,370  
; PRIOR FILING DATE: 1999-12-16  
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; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-732-357A-2

Query Match 100.0%; Score 85; DB 9; Length 331;  
Best Local Similarity 100.0%; Pred. No. 8.7e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 77 HSSDYSWVRKNQYVS 91  
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RESULT 8  
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; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Baton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C11  
; CURRENT APPLICATION NUMBER: US/09/978,295A  
; CURRENT FILING DATE: 2001-10-15  
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; PRIOR FILING DATE: 2001-07-30  
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; PRIOR FILING DATE: 1998-03-10  
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; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 85; DB 9; Length 331;  
Best Local Similarity 100.0%; Pred. No. 8.7e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSSDYSWVRKNQYVS 15  
Db 77 HSSDYSWVRKNQYVS 91

RESULT 9  
US-09-938-418-8  
; Sequence 8, Application US/09938418  
; Patent No. US20020161199A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Polakis, Paul  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Wu, Thomas D.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
; TITLE OF INVENTION: TREATMENT OF TUMOR  
; FILE REFERENCE: P5009R1  
; CURRENT APPLICATION NUMBER: US/09/938,418  
; CURRENT FILING DATE: 2001-08-23  
; PRIOR APPLICATION NUMBER: 60/081,071  
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; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/103,679

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; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 10
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; ORGANISM: Homo Sapien
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US-09-938-418-8

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Query Match      100.0%; Score 85; DB 9; Length 331;
Best Local Similarity 100.0%; Pred. No. 8.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 77 HSSDYSMRKNQYVS 91

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RESULT 10

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US-09-978-697-236
; Sequence 236, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.

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; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C27
; CURRENT APPLICATION NUMBER: US/09/978,697
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
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Query Match 100.0%; Score 85; DB 9; Length 331;  
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Qy 1 HSSDYSMWRKNQYVS 15  
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 Db 77 HSSDYSMWRKNQYVS 91

RESULT 11  
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 ; APPLICANT: Botstein, David  
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 ; APPLICANT: Kuo, Sophia S.  
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 ; APPLICANT: Pan, James;  
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 ; APPLICANT: Shelton, David L.  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, P. Mickey

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; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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Query Match 100.0%; Score 85; DB 9; Length 331;

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Qy 1 HSSDYSMRKNQYVS 15  
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RESULT 12

US-09-999-832A-236  
 ; Sequence 236, Application US/09999832A  
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 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnovers, Luc  
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 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; TITLE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2630P1C53  
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; PRIOR APPLICATION NUMBER: 60/082797  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082796  
; PRIOR FILING DATE: 1998-04-23  
; PRIOR APPLICATION NUMBER: 60/083336  
; PRIOR FILING DATE: 1998-04-27  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/083392  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083495  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083496  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083499  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083545  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083554  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083558  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083559  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083500  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083742  
; PRIOR FILING DATE: 1998-04-30  
; PRIOR APPLICATION NUMBER: 60/084366  
; PRIOR FILING DATE: 1998-05-05  
; PRIOR APPLICATION NUMBER: 60/084414  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/084441  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/084637  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084639  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084640  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084598  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084627  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084643  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/085339  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085338

; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085323  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085582  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085700  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085689  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085580  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 85; DB 9; Length 331;  
Best Local Similarity 100.0%; Pred. No. 8.7e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSSDYSMRKNQYVS 15  
Db 77 HSSDYSMRKNQYVS 91  
|||||

## RESULT 13

US-09-978-189-236  
; Sequence 236, Application US/09978189  
; Publication No. US20030004102A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C7  
; CURRENT APPLICATION NUMBER: US/09/978,189  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13



;; PRIOR APPLICATION NUMBER: 60/085689  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085579  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085580  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085573  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 85; DB 10; Length 331;  
Best Local Similarity 100.0%; Pred. No. 8.7e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSSDYSMWRKNQYVS 15  
Db 77 HSSDYSMWRKNQYVS 91

## RESULT 14

US-09-978-608A-236  
; Sequence 236, Application US/09978608A  
; Publication No. US20030045462A1

## ; GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi  
;; APPLICANT: Baker Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Deanoyers, Luc  
;; APPLICANT: Eaton, Dan  
;; APPLICANT: Ferrara, Napoleon  
;; APPLICANT: Filvaroff, Ellen  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gao, Wei-Qiang  
;; APPLICANT: Gerritsen, Hanspeter  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Hillan, Kenneth J  
;; APPLICANT: Kijavin, Ivar J.  
;; APPLICANT: Kuo, Sophia S.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Shelton, David L.  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Williams, P. Mickey

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; TITLE OF INVENTION: Acids Encoding the Same

;; FILE REFERENCE: P2630P1C22

;; CURRENT APPLICATION NUMBER: US/09/978,608A

;; CURRENT FILING DATE: 2001-10-16

;; NUMBER OF SEQ ID NOS: 624

;; Prior Application removed - See File Wrapper or Palm

;; SEQ ID NO 236

;; LENGTH: 331

;; TYPE: PRT

;; ORGANISM: Homo sapiens

US-09-978-608A-236

Query Match 100.0%; Score 85; DB 10; Length 331;  
Best Local Similarity 100.0%; Pred. No. 8.7e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSSDYSMWRKNQYVS 15  
Db 77 HSSDYSMWRKNQYVS 91

## RESULT 15

US-09-978-585A-236  
; Sequence 236, Application US/09978585A  
; Publication No. US20030049633A1

## ; GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi  
;; APPLICANT: Baker Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Deanoyers, Luc  
;; APPLICANT: Eaton, Dan  
;; APPLICANT: Ferrara, Napoleon  
;; APPLICANT: Filvaroff, Ellen  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gao, Wei-Qiang  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerritsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Hillan, Kenneth J  
;; APPLICANT: Kijavin, Ivar J.  
;; APPLICANT: Kuo, Sophia S.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James;  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Shelton, David L.  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Williams, P. Mickey

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; TITLE OF INVENTION: Acids Encoding the Same

;; FILE REFERENCE: P2630P1C15

;; CURRENT APPLICATION NUMBER: US/09/978,585A

;; CURRENT FILING DATE: 2001-10-16

;; NUMBER OF SEQ ID NOS: 624

;; Prior Application removed - See File Wrapper or Palm

;; SEQ ID NO 236

;; LENGTH: 331

;; TYPE: PRT

;; ORGANISM: Homo sapiens

US-09-978-585A-236

Query Match 100.0%; Score 85; DB 10; Length 331;

Best Local Similarity 100.0%; Pred. No. 8.7e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSSDYSMWRKNQYVS 15

Db 77 HSSDYSMWRKNQYVS 91

Search completed: June 3, 2005, 09:01:04

Job time : 13.35 secs

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# OM protein - protein search, using sw model

Run on: June 3, 2005, 08:10:06 ; Search time 4.1625 Seconds  
(without alignments)  
269.006 Million cell updates/sec

Title: US-10-616-279-10

Perfect score: 85

Sequence: 1 HSSDYSWVRKNQYVS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
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4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	85	100.0	15	4	US-09-732-357B-10
2	85	100.0	330	3	US-09-371-696-2
3	85	100.0	331	2	US-08-799-173A-2
4	85	100.0	331	4	US-09-732-357B-2
5	85	100.0	331	4	US-09-170-042A-2
6	82	96.5	330	4	US-09-732-357B-13
7	52	61.2	299	4	US-09-311-021-202
8	44	51.8	677	4	US-09-270-767-58094
9	44	51.8	847	4	US-09-270-767-42793
10	42	49.4	25	4	US-09-270-767-58735
11	42	49.4	250	4	US-09-248-796A-15562
12	42	49.4	435	3	US-09-072-917A-9
13	42	49.4	877	4	US-09-165-396-5
14	41	48.2	149	4	US-09-270-767-47895
15	41	48.2	297	4	US-09-248-796A-25364
16	40	47.1	111	4	US-09-248-796A-21330
17	40	47.1	114	4	US-09-513-999C-5768
18	40	47.1	456	4	US-09-489-039A-8101
19	40	47.1	462	4	US-09-543-681A-5290
20	40	47.1	742	4	US-09-500-123-12
21	40	47.1	811	4	US-09-500-123-9
22	40	47.1	871	4	US-09-500-123-7
23	40	47.1	1008	4	US-09-949-016-10423
24	39	45.9	152	4	US-09-270-767-37205
25	39	45.9	152	4	US-09-270-767-52422
26	39	45.9	163	4	US-09-328-352-7800
27	39	45.9	249	4	US-09-270-767-43254

28 45.9 281 4 US-09-248-796A-23359 Sequence 23359, A  
29 45.9 635 4 US-09-248-796A-16944 Sequence 16944, A  
30 45.9 1085 1 US-08-431-080-28 Sequence 28, Appl  
31 45.9 1085 2 US-08-938-534-28 Sequence 28, Appl  
32 45.9 1085 3 US-09-345-294-28 Sequence 28, Appl  
33 45.9 1169 1 US-08-542-921-2 Sequence 2, Appli  
34 45.9 1169 2 US-08-880-685-2 Sequence 2, Appli  
35 45.9 1169 2 US-08-880-684-2 Sequence 2, Appli  
36 38.5 45.3 404 4 US-09-248-796A-19544 Sequence 19544, A  
37 38 44.7 126 4 US-09-755-665-27 Sequence 27, Appl  
38 38 44.7 133 4 US-09-755-665-4 Sequence 4, Appli  
39 38 44.7 172 4 US-08-737-109-17 Sequence 17, Appl  
40 38 44.7 185 4 US-09-248-796A-14213 Sequence 14213, A  
41 38 44.7 319 4 US-09-107-532A-6215 Sequence 6215, Ap  
42 38 44.7 321 3 US-08-915-795-9 Sequence 9, Appli  
43 38 44.7 321 4 US-09-847-524-4 Sequence 4, Appli  
44 38 44.7 321 4 US-09-296-275-9 Sequence 9, Appli  
45 38 44.7 325 3 US-08-915-795-3 Sequence 3, Appli

## ALIGNMENTS

RESULT 1  
US-09-732-357B-10  
; Sequence 10, Application US/09732357B  
; Patent No. 6682902  
; GENERAL INFORMATION:  
; APPLICANT: Harkins, Richard  
; APPLICANT: Parkes, Deborah  
; APPLICANT: Parry, Gordon  
; APPLICANT: Schneider, Douglas  
; APPLICANT: Steindbrecher, Renate  
; TITLE OF INVENTION: DNA Encoding a No. 6682902el RG-1 Polypeptide  
; FILE REFERENCE: 51791AUSM1  
; CURRENT APPLICATION NUMBER: US/09732,357B  
; CURRENT FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: US 60/172,370  
; PRIOR FILING DATE: 1999-12-16  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-732-357B-10

Query Match 100.0%; Score 85; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSSDYSWVRKNQYVS 15  
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Db 1 HSSDYSWVRKNQYVS 15

RESULT 2  
US-09-371-696-2  
; Sequence 2, Application US/09371696  
; Patent No. 6287777  
; GENERAL INFORMATION:  
; APPLICANT: Sytkowski, Arthur J.  
; APPLICANT: Yang, Meiheng  
; TITLE OF INVENTION: NOVEL NPG-1 GENE THAT IS DIFFERENTIALLY EXPRESSED IN PROSTATE  
; FILE REFERENCE: 01948/033002  
; CURRENT APPLICATION NUMBER: US/09/371,696  
; CURRENT FILING DATE: 1999-08-10  
; EARLIER APPLICATION NUMBER: US 09/022,238  
; EARLIER FILING DATE: 1998-02-11  
; EARLIER APPLICATION NUMBER: US 08/644,326  
; EARLIER FILING DATE: 1996-05-10  
; NUMBER OF SEQ ID NOS: 5



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; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-732-357B-13

Query Match      96.5%; Score 82; DB 4; Length 330;
Best Local Similarity 93.3%; Pred. No. 1.4e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSSDYSWVRKNQYVS 15
Db 76 HSSDYSWVRKNQYVS 90
|||||:|||||

RESULT 7
US-09-311-021-202
; Sequence 202, Application US/09311021
; Patent No. 6706869
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fectel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6300-11A
; CURRENT APPLICATION NUMBER: US/09/311,021
; CURRENT FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 202
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-311-021-202

Query Match      61.2%; Score 52; DB 4; Length 299;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MVRKNQYVS 15
Db 1 MVRKNQYVS 9
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RESULT 8
US-09-270-767-58094
; Sequence 58094, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58094
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-58094

Query Match      51.8%; Score 44; DB 4; Length 677;
Best Local Similarity 46.7%; Pred. No. 41;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 HSSDYSWVRKNQYVS 15
Db 230 HSSDYRFWESGELAS 244
|||||:|:|

RESULT 9
US-09-270-767-42783
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; Sequence 42783, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42783
; LENGTH: 847
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-42783

Query Match      51.8%; Score 44; DB 4; Length 847;
Best Local Similarity 46.7%; Pred. No. 51;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 HSSDYSWVRKNQYVS 15
Db 230 HSSDYRFWESGELAS 244
|||||:|:|

RESULT 10
US-09-270-767-58735
; Sequence 58735, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58735
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-58735

Query Match      49.4%; Score 42; DB 4; Length 25;
Best Local Similarity 63.6%; Pred. No. 2.8;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HSSDYSWVRKN 11
Db 5 HSSDYSLKKRN 15
|||||:|:|

RESULT 11
US-09-248-796A-15562
; Sequence 15562, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15562
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-15562
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Query Match 49.4%; Score 42; DB 4; Length 250;  
Best Local Similarity 40.0%; Pred. No. 31;  
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 HSSDYSWVRKNQYV 15  
Db 209 HDSEFDLSRNTYIS 223

RESULT 12  
US-09-072-917A-9  
; Sequence 9, Application US/09072917A  
; Patent No. 6288302  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Su-May  
; APPLICANT: Liu, Li-Fei  
; APPLICANT: Chan, Ming-Tsair  
; TITLE OF INVENTION: Application of Alpha-Amylase Gene  
; TITLE OF INVENTION: Promoter and Signal Sequence in the Production of  
; Patent No. 6288302  
; TITLE OF INVENTION: Recombinant Proteins in Transgenic Plants and Transgenic  
; TITLE OF INVENTION: Plant Seeds  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 233 South Wacker Drive/6300 Sears Tower  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/072.917A  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/509,962  
; FILING DATE: 01-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gass, David A.  
; REGISTRATION NUMBER: 38,153  
; REFERENCE/DOCKET NUMBER: 28123/34257  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 435 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-072-917A-9

Query Match 49.4%; Score 42; DB 3; Length 435;  
Best Local Similarity 60.0%; Pred. No. 54;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HSSDYSWVRK 10  
Db 415 HGKDYSVWEK 424

RESULT 13  
US-09-165-396-5  
; Sequence 5, Application US/09165396  
; Patent No. 641134  
; GENERAL INFORMATION:  
; APPLICANT: BECKER, JEFFREY W.

; APPLICANT: LUBKOWITZ, MARK A.  
; TITLE OF INVENTION: ISOLATED CANDIDA ALBICANS OLIGOPEPTIDE TRANSPORTER GENE  
; FILE REFERENCE: 372.6520P  
; CURRENT APPLICATION NUMBER: US/09/165,396  
; CURRENT FILING DATE: 1998-10-02  
; EARLIER APPLICATION NUMBER: PCT/US98/02332  
; EARLIER FILING DATE: 1998-02-06  
; EARLIER APPLICATION NUMBER: 60/037,859  
; EARLIER FILING DATE: 1997-02-07  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 877  
; TYPE: PRT  
; ORGANISM: S. cerevisiae  
; US-09-165-396-5

Query Match 49.4%; Score 42; DB 4; Length 877;  
Best Local Similarity 42.3%; Pred. No. 1.1e+02;  
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 HSSDYSWVRKNQYV 14  
Db 36 HSSDPSQWYDEQI 49

RESULT 14  
US-09-270-767-47885  
; Sequence 47885, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 47885  
; LENGTH: 149  
; TYPE: PRT  
; ORGANISM: *Drosophila melanogaster*  
; US-09-270-767-47885

Query Match 48.2%; Score 41; DB 4; Length 149;  
Best Local Similarity 54.5%; Pred. No. 26;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SDYSWVRKNQY 13  
Db 125 SDYSWVRKNQY 135

RESULT 15  
US-09-248-796A-25364  
; Sequence 25364, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 25364  
; LENGTH: 297  
; TYPE: PRT  
; ORGANISM: *Candida albicans*



US-09-248-796A-25364

Query Match 48.2%; Score 41; DB 4; Length 297;  
Best Local Similarity 50.0%; Pred. No. 53;  
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 4 DYSMWRKNQYVS 15

270 DYSIWKNQLLA 281

Search completed: June 3, 2005, 08:31:27  
Job time : 5.3625 secs

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